

GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: July 9, 2005, 06:30:47 ; Search time 110.427 Seconds

(without alignments)

2295.451 Million cell updates/sec

Title: US-09-776-865-4

Perfect score: 495

Sequence: 1 MKSPVSDLAPSDEEGSDRT.....LPAKGEVQNVNAISDHQGRN 495

Scoring table: Oligo

Gapop 60.0 , Gapext 60.0

Searched: 1612378 seqs, 512079187 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : UniProt 03:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	495	100.0	495	1	S175_SHEEP		Q9mzd1 ovis aries
2	61	12.3	495	1	S175_HUMAN		Q9na2 homo sapien
3	32	6.5	495	1	S175_MOUSE		Q8bn82 mus musculus
4	12	2.4	363	2	Q9BWS1		Q8bn81 mus musculus
5	12	2.4	436	1	NPT3_HUMAN		Q00524 homo sapien
6	12	2.4	447	2	Q8VCX8		Q8vcx8 mus musculus
7	12	2.4	466	2	Q961h1		Q961h1 homo sapien
8	12	2.4	470	2	Q7YTZ7		Q7yz7 drosophila
9	12	2.4	559	2	Q9VY97		Q9vy97 drosophila
10	11	2.2	582	2	Q9P2U8		Q9p2u8 homo sapien
11	11	2.2	582	2	Q920B7		Q920b7 mus musculus
12	11	2.2	582	2	Q8BLE7		Q8ble7 mus musculus
13	11	2.2	582	2	Q9J12		Q9j12 rattus norvegicus
14	10	2.0	390	2	Q921B2		Q921b2 mus musculus
15	10	2.0	465	1	NPT1_MOUSE		Q61983 mus musculus
16	10	2.0	465	1	NPT1_BAT		Q62795 rattus norvegicus
17	10	2.0	465	1	Q8K3H3		Q8k3h3 rattus norvegicus
18	10	2.0	465	2	Q91WV5		Q91wv5 mus musculus
19	10	2.0	465	2	Q6AZ46		Q6az46 rattus norvegicus
20	10	2.0	476	2	Q7Q579		Q7q579 anophelles gambiae
21	10	2.0	497	2	Q6NR28		Q6nr28 drosophila
22	10	2.0	497	2	Q7KRJ1		Q7krj1 drosophila
23	10	2.0	502	2	Q9VDM0		Q9vdm0 drosophila
24	10	2.0	544	1	YRT3_CAEEL		Q10046 caenorhabditis elegans
25	10	2.0	544	2	Q7Q580		Q7q58 anophelles gambiae
26	10	2.0	573	2	Q09932		Q09932 caenorhabditis elegans
27	9	1.8	69	2	Q91Y99		Q91y99 mus musculus
28	9	1.8	127	2	Q71118		Q71118 trichoplax adhaerens
29	9	1.8	395	2	Q65502		Q65502 arabidopsis thaliana
30	9	1.8	469	2	Q8CJH8		Q8cjh8 rattus norvegicus
31	9	1.8	475	2	Q6AZ69		Q6az69 rattus norvegicus

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5	12	2.4	436	1	NPT3_HUMAN		Q00524 homo sapien
6	12	2.4	447	2	Q8VCX8		Q8vcx8 mus musculus
7	12	2.4	466	2	Q961h1		Q961h1 homo sapien
8	12	2.4	470	2	Q7YTZ7		Q7yz7 drosophila
9	12	2.4	559	2	Q9VY97		Q9vy97 drosophila
10	11	2.2	582	2	Q9P2U8		Q9p2u8 homo sapien
11	11	2.2	582	2	Q920B7		Q920b7 mus musculus
12	11	2.2	582	2	Q8BLE7		Q8ble7 mus musculus
13	11	2.2	582	2	Q9J12		Q9j12 rattus norvegicus
14	10	2.0	390	2	Q921B2		Q921b2 mus musculus
15	10	2.0	465	1	NPT1_MOUSE		Q61983 mus musculus
16	10	2.0	465	1	NPT1_BAT		Q62795 rattus norvegicus
17	10	2.0	465	1	Q8K3H3		Q8k3h3 rattus norvegicus
18	10	2.0	465	2	Q91WV5		Q91wv5 mus musculus
19	10	2.0	465	2	Q6AZ46		Q6az46 rattus norvegicus
20	10	2.0	476	2	Q7Q579		Q7q579 anophelles gambiae
21	10	2.0	497	2	Q6NR28		Q6nr28 drosophila
22	10	2.0	497	2	Q7KRJ1		Q7krj1 drosophila
23	10	2.0	502	2	Q9VDM0		Q9vdm0 drosophila
24	10	2.0	544	1	YRT3_CAEEL		Q10046 caenorhabditis elegans
25	10	2.0	544	2	Q7Q580		Q7q58 anophelles gambiae
26	10	2.0	573	2	Q09932		Q09932 caenorhabditis elegans
27	9	1.8	69	2	Q91Y99		Q91y99 mus musculus
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18	10	2.0</					

105	8	1.6	223	2	034899	littorina h	178	8	1.6	303	2	Q71bt0	blackburnia
106	8	1.6	223	2	034906	littorina k	179	8	1.6	308	1	LIVH_SALTY	
107	8	1.6	223	2	034906	littorina l	180	8	1.6	311	2	Q71br7	blackburnia
108	8	1.6	223	2	034914	littorina m	181	8	1.6	311	2	Q71bt4	blackburnia
109	8	1.6	223	2	034914	littorina m	182	8	1.6	316	2	Q71bs5	blackburnia
110	8	1.6	223	2	034924	littorina o	183	8	1.6	316	2	Q71bs7	blackburnia
111	8	1.6	223	2	034933	littorina p	184	8	1.6	316	2	Q71ls6	oryza sativ
112	8	1.6	223	2	034934	littorina s	185	8	1.6	320	2	Q71bs4	blackburnia
113	8	1.6	223	2	07GG43	littorina s	186	8	1.6	321	2	Q71bs9	oryza sativ
114	8	1.6	226	2	09B388	littorina s	187	8	1.6	326	2	Q9B707	eurycea wat
115	8	1.6	228	2	08LvZ9	littorina s	188	8	1.6	327	2	Q71br1	blackburnia
116	8	1.6	232	2	09M376	littorina s	189	8	1.6	327	2	Q71br3	blackburnia
117	8	1.6	237	2	003761	littorina s	190	8	1.6	327	2	Q71br5	blackburnia
118	8	1.6	238	2	003745	littorina s	191	8	1.6	327	2	Q71br6	blackburnia
119	8	1.6	238	2	003750	littorina s	192	8	1.6	327	2	Q71bs8	blackburnia
120	8	1.6	238	2	003760	littorina s	193	8	1.6	327	2	Q71bu3	blackburnia
121	8	1.6	238	2	09GCH1	littorina s	194	8	1.6	328	2	Q71br2	blackburnia
122	8	1.6	238	2	09GCH2	littorina s	195	8	1.6	329	2	Q71bs1	blackburnia
123	8	1.6	238	2	09GCH3	littorina s	196	8	1.6	329	2	Q71br4	blackburnia
124	8	1.6	238	2	09GCH4	littorina s	197	8	1.6	330	2	Q71bs6	blackburnia
125	8	1.6	238	2	09GCH5	littorina s	198	8	1.6	332	2	Q9B706	eurycea wat
126	8	1.6	238	2	09GCH6	littorina s	199	8	1.6	332	2	Q71bt1	blackburnia
127	8	1.6	238	2	09GCH7	littorina s	200	8	1.6	333	2	Q71br3	blackburnia
128	8	1.6	238	2	09GCH8	littorina s	201	8	1.6	338	2	Q71br2	blackburnia
129	8	1.6	238	2	09GCH9	littorina s	202	8	1.6	338	2	Q71br4	blackburnia
130	8	1.6	238	2	09GCI0	littorina s	203	8	1.6	338	2	Q71bs6	blackburnia
131	8	1.6	238	2	09GCI1	littorina s	204	8	1.6	338	2	Q7Xwf4	oryza sativ
132	8	1.6	238	2	09GCI2	littorina s	205	8	1.6	339	2	Q7Xuh8	oryza sativ
133	8	1.6	238	2	09GCI3	littorina s	206	8	1.6	341	2	Q9B710	eurycea tro
134	8	1.6	238	2	09GCI4	littorina s	207	8	1.6	342	2	Q24438	caenorhabdi
135	8	1.6	238	2	09GCI5	littorina s	208	8	1.6	358	2	Q71bu7	blackburnia
136	8	1.6	238	2	09GCI6	littorina s	209	8	1.6	359	2	Q17100	caenorhabdi
137	8	1.6	239	2	003746	littorina can	210	8	1.6	364	2	Q71bt9	blackburnia
138	8	1.6	239	2	09GCI12	scathophaga	211	8	1.6	364	2	Q71bu0	blackburnia
139	8	1.6	239	2	003748	scathophaga	212	8	1.6	364	2	Q71bu4	blackburnia
140	8	1.6	239	2	003749	scathophaga	213	8	1.6	364	2	Q71bu9	blackburnia
141	8	1.6	239	2	003752	scathophaga	214	8	1.6	364	2	Q71bv0	blackburnia
142	8	1.6	239	2	003753	scathophaga	215	8	1.6	365	1	GLE2_YEAST	
143	8	1.6	239	2	003757	scathophaga	216	8	1.6	369	2	Q72kC7	thermus the
144	8	1.6	239	2	003758	scathophaga	217	8	1.6	371	2	Q71bu0	blackburnia
145	8	1.6	239	2	003759	scathophaga	218	8	1.6	371	2	Q8Hq06	thrips img
146	8	1.6	243	2	075yp1	nesiohelix	219	8	1.6	372	2	Q6QRA1	eurycea tyn
147	8	1.6	248	2	08M111	harpagifer	220	8	1.6	372	2	Q6QRE2	eurycea tyn
148	8	1.6	255	2	09B394	blackburnia	221	8	1.6	372	2	Q6QRE2	eurycea mul
149	8	1.6	257	2	09B624	oryza sativ	222	8	1.6	372	2	Q71bu2	blackburnia
150	8	1.6	258	2	07XL7	oryza sativ	223	8	1.6	378	1	CYB_ANOGA	
151	8	1.6	260	2	09B380	blackburnia	224	8	1.6	378	1	CYB_ANOQU	
152	8	1.6	260	2	09B381	blackburnia	225	8	1.6	378	2	Q8H6E0	
153	8	1.6	260	2	09B389	blackburnia	226	8	1.6	378	2	Q6B3B1	pteranorcy
154	8	1.6	260	2	09B391	blackburnia	227	8	1.6	380	1	CYB_CEPNE	
155	8	1.6	260	2	09B395	blackburnia	228	8	1.6	380	2	Q9B2C3	
156	8	1.6	260	2	09B518	blackburnia	229	8	1.6	380	2	Q9GGM6	
157	8	1.6	260	2	09B3A4	blackburnia	230	8	1.6	380	2	Q9GDM7	
158	8	1.6	260	2	09B3B0	blackburnia	231	8	1.6	380	2	Q64A1	
159	8	1.6	260	2	09B3B7	blackburnia	232	8	1.6	380	2	Q644K5	
160	8	1.6	260	2	09B3C2	blackburnia	233	8	1.6	380	2	Q645C5	
161	8	1.6	260	2	09B3C7	blackburnia	234	8	1.6	381	2	Q35424	protocerpterus
162	8	1.6	260	2	09B5d0	blackburnia	235	8	1.6	402	2	Q7T0H3	
163	8	1.6	269	2	08S2T4	pyrococcus	236	8	1.6	454	2	Q8Y0F1	
164	8	1.6	269	2	09B3D3	pyrococcus	237	8	1.6	465	1	NPT1_RABIT	
165	8	1.6	269	2	09B3D6	pyrococcus	238	8	1.6	465	2	Q8VZ70	
166	8	1.6	269	2	09B3D9	pyrococcus	239	8	1.6	476	2	Q8ZER7	
167	8	1.6	269	2	058366	pyrococcus	240	8	1.6	479	1	DBPA_BASU	
168	8	1.6	269	2	08S691	oryza sativ	241	8	1.6	494	2	Q83SH5	
169	8	1.6	269	2	07G785	oryza sativ	242	8	1.6	497	2	Q9Y2C5	
170	8	1.6	269	2	07XLQ9	oryza sativ	243	8	1.6	498	2	Q8VCI5	
171	8	1.6	269	2	0851B3	oryza sativ	244	8	1.6	502	2	Q7XCB6	
172	8	1.6	269	2	0851b5	oryza sativ	245	8	1.6	515	2	Q8JFT2	
173	8	1.6	284	2	06DU58	oryza sativ	246	8	1.6	535	2	Q7PwK4	
174	8	1.6	291	2	08LHH8	oryza sativ	247	8	1.6	560	2	Q6Pcd0	
175	8	1.6	291	2	07XXK8	oryza sativ	248	8	1.6	560	2	Q9PPU7	
176	8	1.6	299	2	07XXK6	oryza sativ	249	8	1.6	560	2	Q62634	
177	8	1.6	300	2	Q33966	brachylophu	250	8	1.6	576	2	Q6inc8	

GenCore version 5.1.6  
(c) 1993 - 2005 Compugen Ltd.

## OM protein - protein search, using sw model

Run on: July 9, 2005, 06:34:43 ; Search time 24.9661 Seconds

(without alignments)

1907.682 Million cell updates/sec

Title: US-09-776-865-4

Perfect score: 495

Sequence: 1 MKSPVSDIAPSDEEGESDRT.....LFAGKEVQNNWAISDHGHRN 495

Scoring table: OLIGO

Gapext 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post processing: Listing first 1000 summaries

Database : PIR 79:\*

1: Piri1:\*

2: Piri2:\*

3: Piri3:\*

4: Piri4:\*

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## SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	10	2.0	465	2	S69915		sodium-phosphate t
2	10	2.0	544	2	T24633		hypothetical prote
3	10	2.0	573	2	T23589		hypothetical prote
4	9	1.8	380	2	T29248		hypothetical prote
5	9	1.8	395	2	T06132		hypothetical prote
6	8	1.6	138	2	E97587		diacylglycerol kin
7	8	1.6	138	2	AG2808		diacylglycerol kin
8	8	1.6	269	1	H71107		gufa protein homol
9	8	1.6	308	2	AG0992		high-affinity bran
10	8	1.6	308	2	JH0668		high-affinity bran
11	8	1.6	359	2	T32619		hypothetical prote
12	8	1.6	365	2	S50610		hypothetical prote
13	8	1.6	378	2	T12009		ubiquinol-cytochro
14	8	1.6	378	2	T09812		ubiquinol-cytochro
15	8	1.6	380	2	T11381		ubiquinol-cytochro
16	8	1.6	381	2	S68140		hypothetical prote
17	8	1.6	396	2	T32619		hypothetical prote
18	8	1.6	465	2	A56410		sodium/phosphate t
19	8	1.6	479	2	F69613		ATP-dependent RNA
20	8	1.6	560	2	T12514		brain specific Na+
21	8	1.6	837	2	AF2031		hypothetical prote
22	8	1.6	1287	2	JC6306		two-component hydr
23	8	1.6	4128	2	A60704		protein kinase (EC
24	7	1.4	25	2			serine proteinase
25	7	1.4	33	2	S13863		dihydrofolipoamide d
26	7	1.4	44	2	A21124		hypothetical prote
27	7	1.4	55	2	A21124		Sxr (Bkm-homolog)
28	7	1.4	68	2	E64161		YacG protein homol
29	7	1.4	126	2	F82072		holo-(acyl-carrier

30	1.4	31	2	G97824		50S ribosomal prot
31	1.4	32	2	S09525		mercury transport
32	1.4	33	2	PT0433		progesterone 11 $\alpha$ l
33	1.4	34	2	E82330		conserved hypoth
34	1.4	35	2	C97624		pet protein (imp)
35	1.4	36	2	AD2847		transcription regu
36	1.4	37	2	OLBO4		cytochrome-c oxida
37	1.4	38	2	AH2313		phosphatidylglycer
38	1.4	39	2	T17625		hypothetical prote
39	1.4	40	2	JK0021		somatotropin - ski
40	1.4	41	2	A61123		somatotropin - Moz
41	1.4	42	2	PC1082		somatotropin - Jap
42	1.4	43	2	JU0030		somatotropin - yel
43	1.4	44	2	PC1088		somatotropin - dus
44	1.4	45	2	PC1087		somatotropin - gre
45	1.4	46	2	A13437		somatotropin - hypoth
46	1.4	47	2	A70750		colicin v product
47	1.4	48	2	S00747		hypothetical prote
48	1.4	49	2	STFI		somatotropin precu
49	1.4	50	2	A56642		somatotropin precu
50	1.4	51	2	T51289		somatotropin precu
51	1.4	52	2	JN0484		somatotropin precu
52	1.4	53	2	JH0577		somatotropin precu
53	1.4	54	2	A56904		somatotropin precu
54	1.4	55	2	S30491		somatotropin - Aca
55	1.4	56	2	JC4261		somatotropin precu
56	1.4	57	2	S01746		somatotropin precu
57	1.4	58	2	C70898		hypothetical prote
58	1.4	59	2	B83083		hypothetical prote
59	1.4	60	2	JC6201		conserved hypothet
60	1.4	61	2	S42059		GS1 protein homolo
61	1.4	62	2	AE2314		TEGT protein - rat
62	1.4	63	2	A28259		ATP-binding protei
63	1.4	64	2	S72859		hypothetical prote
64	1.4	65	2	E90184		conserved hypothet
65	1.4	66	2	B82040		general secretion
66	1.4	67	2	E64109		dimethylsulfoxide
67	1.4	68	2	H70855		hypothetical prote
68	1.4	69	2	E95128		conserved hypothet
69	1.4	70	2	B79799		hypothetical prote
70	1.4	71	2	I76721		hypothetical prote
71	1.4	72	2	S60666		probable ATP-bindi
72	1.4	73	2	G85984		hypothetical prote
73	1.4	74	2	D91139		hypothetical prote
74	1.4	75	2	AB0436		conserved hypothet
75	1.4	76	2	S74771		hypothetical prote
76	1.4	77	2	G64167		hypothetical prote
77	1.4	78	2	AB0762		conserved hypothet
78	1.4	79	2	H64438		UDP-N-acetylglucos
79	1.4	80	2	H75081		phosphate abc tran
80	1.4	81	2	H75285		probable phospho
81	1.4	82	2	E91206		probable ARAC-type
82	1.4	83	2	G86052		probable ARAC-type
83	1.4	84	2	E65170		hypothetical prote
84	1.4	85	2	G98084		hypothetical prote
85	1.4	86	2	G95220		hypothetical prote
86	1.4	87	2	S11151		amid protein - Str
87	1.4	88	2	B71330		NADH2 dehydrogenas
88	1.4	89	2	E64426		Phosphate transpor
89	1.4	90	2	T70768		hypothetical prote
90	1.4	91	2	T11337		NADH2 dehydrogenas
91	1.4	92	2	QXB0M		NADH2 dehydrogenas
92	1.4	93	2	A58886		NADH2 dehydrogenas
93	1.4	94	2	S47870		NADH2 dehydrogenas
94	1.4	95	2	T11438		NADH2 dehydrogenas
95	1.4	96	2	T11441		NADH2 dehydrogenas
96	1.4	97	2	T11140		NADH2 dehydrogenas
97	1.4	98	2	T11493		NADH2 dehydrogenas
98	1.4	99	2	T11402		NADH2 dehydrogenas
99	1.4	100	2	S41835		NADH2 dehydrogenas
100	1.4	101	2	S26151		NADH2 dehydrogenas
101	1.4	102	2	A58850		NADH2 dehydrogenas

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104	7	318	2	T45550	177	7	1.4	563	
105	7	318	2	T11363	178	7	1.4	576	
106	7	1.4	318	2	T11857	179	7	1.4	576
107	7	1.4	318	2	T11247	180	7	1.4	600
108	7	1.4	318	2	T10972	181	7	1.4	635
109	7	1.4	318	2	T11050	182	7	1.4	640
110	7	1.4	321	2	T13811	183	7	1.4	644
111	7	1.4	321	2	S55004	184	7	1.4	644
112	7	1.4	321	2	A6775	185	7	1.4	644
113	7	1.4	322	2	S68128	186	7	1.4	644
114	7	1.4	323	1	QXXL1M	187	7	1.4	648
115	7	1.4	323	2	T11793	188	7	1.4	663
116	7	1.4	323	2	A34284	189	7	1.4	663
117	7	1.4	323	2	A58892	190	7	1.4	674
118	7	1.4	323	2	T09857	191	7	1.4	678
119	7	1.4	323	2	T11820	192	7	1.4	682
120	7	1.4	324	2	S36002	193	7	1.4	752
121	7	1.4	324	2	S35462	194	7	1.4	768
122	7	1.4	324	2	T09947	195	7	1.4	778
123	7	1.4	324	2	C41608	196	7	1.4	781
124	7	1.4	324	2	D87075	197	7	1.4	791
125	7	1.4	326	1	S41120	198	7	1.4	847
126	7	1.4	326	2	T36494	199	7	1.4	860
127	7	1.4	330	2	A40602	200	7	1.4	877
128	7	1.4	333	2	E97368	201	7	1.4	909
129	7	1.4	338	2	AD2586	202	7	1.4	924
130	7	1.4	343	2	T14245	203	7	1.4	925
131	7	1.4	351	2	T19622	204	7	1.4	928
132	7	1.4	370	2	AB0602	205	7	1.4	928
133	7	1.4	372	2	S52054	206	7	1.4	949
134	7	1.4	372	2	S20056	207	7	1.4	1005
135	7	1.4	373	2	T137463	208	7	1.4	1018
136	7	1.4	377	2	F95982	209	7	1.4	1082
137	7	1.4	381	2	T29300	210	7	1.4	1082
138	7	1.4	384	2	A70805	211	7	1.4	1083
139	7	1.4	389	2	T10194	212	7	1.4	1085
140	7	1.4	390	2	T50037	213	7	1.4	1085
141	7	1.4	397	2	S23909	214	7	1.4	1208
142	7	1.4	407	2	F70696	215	7	1.4	1225
143	7	1.4	407	2	S74951	216	7	1.4	1325
144	7	1.4	410	2	C82912	217	7	1.4	1436
145	7	1.4	422	2	A422	218	7	1.4	1516
146	7	1.4	422	2	G726654	219	7	1.4	1538
147	7	1.4	436	2	C69764	220	7	1.4	1538
148	7	1.4	443	2	S77166	221	7	1.4	1538
149	7	1.4	448	2	T12005	222	7	1.4	1943
150	7	1.4	452	2	T35729	223	7	1.4	1969
151	7	1.4	454	2	G70797	224	7	1.4	2145
152	7	1.4	454	2	T26654	225	7	1.4	3194
153	7	1.4	455	2	A82957	226	7	1.4	15281
154	7	1.4	460	2	D80968	227	6	1.2	13
155	7	1.4	461	2	D84971	228	6	1.2	2
156	7	1.4	462	2	E32840	229	6	1.2	44
157	7	1.4	463	2	E64476	230	6	1.2	45
158	7	1.4	465	2	T139473	231	6	1.2	50
159	7	1.4	467	2	A48916	232	6	1.2	50
160	7	1.4	472	2	S28286	233	6	1.2	52
161	7	1.4	473	2	S20612	234	6	1.2	55
162	7	1.4	473	2	A38627	235	6	1.2	56
163	7	1.4	477	2	H83588	236	6	1.2	57
164	7	1.4	479	2	E91195	237	6	1.2	59
165	7	1.4	479	2	F86042	238	6	1.2	59
166	7	1.4	479	2	C65167	239	6	1.2	52
167	7	1.4	487	2	F72200	240	6	1.2	55
168	7	1.4	493	2	G88553	241	6	1.2	56
169	7	1.4	508	2	T6156	242	6	1.2	57
170	7	1.4	515	2	E71447	243	6	1.2	59
171	7	1.4	521	2	A53153	244	6	1.2	60
172	7	1.4	528	2	AG1937	245	6	1.2	61
173	7	1.4	531	2	T12407	246	6	1.2	61
174	7	1.4	539	2	F72288	247	6	1.2	61
175	7	1.4	542	1	A70220	248	6	1.2	62

GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: July 9, 2005, 06:55:49 ; Search time 106.586 Seconds  
 (without alignments)

1794.174 Million cell updates/sec

Title: US-09-776-865-4

Perfect score: 495

Sequence: 1 MKSPVSDLAPSDEEGESDRT.....LPAKGEVQNWAISDHGHRN 495

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1726216 seqs, 386330316 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1726216

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Published Applications AA:\*

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 13 12 14 US-10-029-386-27708 Sequence 27708, A  
 14 11 2.2 578 9 US-09-740-041-4 Sequence 4, App1  
 15 11 2.2 578 14 US-10-389-967-4 Sequence 4, App1  
 16 11 2.2 582 9 US-09-915-181A-4 Sequence 4, App1  
 17 11 2.2 582 15 US-10-205-331-7 Sequence 7, App1  
 18 11 2.2 582 16 US-10-734-731-10 Sequence 10, App1  
 19 11 2.2 582 16 US-10-734-731-12 Sequence 12, App1  
 20 11 2.2 582 16 US-10-734-731-14 Sequence 14, App1  
 21 11 2.2 582 16 US-10-807-500-10 Sequence 12, App1  
 22 11 2.2 582 16 US-10-807-500-12 Sequence 12, App1  
 23 11 2.0 582 16 US-10-807-500-14 Sequence 14, App1  
 24 10 2.0 544 15 US-10-369-493-5873 Sequence 8, App1  
 25 10 2.0 573 15 US-10-369-493-5871 Sequence 8, App1  
 26 10 2.0 573 15 US-10-369-493-5872 Sequence 8, App1  
 27 10 2.0 1803 16 US-10-437-963-18751 Sequence 188751,  
 28 9 1.8 71 16 US-10-425-115-288336 Sequence 288336,  
 29 8 1.6 78 16 US-10-437-963-154917 Sequence 154917,  
 30 8 1.6 93 16 US-10-425-115-166597 Sequence 366597,  
 31 8 1.6 122 14 US-10-312-187-12 Sequence 12, App1  
 32 8 1.6 124 16 US-10-425-115-317259 Sequence 317259,  
 33 8 1.6 143 16 US-10-425-115-35986 Sequence 335986,  
 34 8 1.6 232 15 US-10-425-114-43907 Sequence 156319, A  
 35 8 1.6 235 15 US-10-282-122A-56379 Sequence 328L, App  
 36 8 1.6 264 15 US-10-108-260A-3281 Sequence 130004,  
 37 8 1.6 269 16 US-10-437-963-130004 Sequence 138193,  
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 58 8 1.6 560 16 US-09-915-181A-8 Sequence 8, App11  
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 60 8 1.6 560 15 US-10-311-790-5 Sequence 4, App11  
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 72 8 1.6 580 16 US-10-437-963-146162 Sequence 146162,  
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 74 8 1.6 589 18 US-10-437-963-1731-28 Sequence 28, App11  
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 76 8 1.6 594 18 US-10-437-963-124551 Sequence 46, App11  
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 79 8 1.6 642 16 US-10-437-963-164012 Sequence 164012,  
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 81 8 1.6 652 16 US-10-437-963-124115 Sequence 124115,  
 82 8 1.6 656 16 US-10-437-963-141761 Sequence 141761,  
 83 8 1.6 656 17 US-10-437-963-141769 Sequence 141769,

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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1	495	100.0	495	9	US-09-776-865-4	Sequence 4, App1
2	495	100.0	495	17	US-10-823-506-4	Sequence 4, App1
3	61	12.3	194	15	US-10-296-115-1200	Sequence 1200, App1
4	61	12.3	272	15	US-10-264-049-2351	Sequence 2351, App1
5	61	12.3	284	15	US-10-264-049-2477	Sequence 2477, App1
6	61	12.3	495	9	US-09-915-181A-7	Sequence 7, App1
7	61	12.3	495	16	US-10-755-889-588	Sequence 588, App1
8	61	12.3	495	17	US-10-823-506-2	Sequence 2, App1
9	61	12.3	536	9	US-09-776-865-2	Sequence 2, App1
10	61	12.3	536	17	US-10-823-506-8	Sequence 8, App1
11	14	2.8	495	17	US-10-823-506-10	Sequence 10, App1

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86	8	US-10-437-963-130226	Sequence 110226,	Sequence 107824,
87	8	US-10-437-963-141764	Sequence 141764,	Sequence 10264,
88	8	US-10-437-963-124150	Sequence 124150,	Sequence 188693,
89	8	US-10-437-963-107799	Sequence 107799,	Sequence 188682,
90	8	US-10-437-963-130194	Sequence 130194,	Sequence 101687,
91	8	US-10-437-963-130258	Sequence 130258,	Sequence 188585,
92	8	US-10-437-963-141741	Sequence 141741,	Sequence 107735,
93	8	US-10-437-963-141727	Sequence 141727,	Sequence 134262,
94	8	US-10-437-963-107890	Sequence 107890,	Sequence 188666,
95	8	US-10-437-963-130227	Sequence 130227,	Sequence 107688,
96	8	US-10-437-963-130255	Sequence 130255,	Sequence 107778,
97	8	US-10-437-963-154809	Sequence 154809,	Sequence 188627,
98	8	US-10-437-963-107643	Sequence 107643,	Sequence 188576,
99	8	US-10-437-963-124149	Sequence 124149,	Sequence 107640,
100	8	US-10-437-963-138194	Sequence 138194,	Sequence 188747,
101	8	US-10-437-963-124145	Sequence 124145,	Sequence 188717,
102	8	US-10-437-963-130182	Sequence 130182,	Sequence 188567,
103	8	US-10-437-187-3	Sequence 3, Appli,	Sequence 188725,
104	8	US-10-437-963-130191	Sequence 130191,	Sequence 130233,
105	8	US-09-915-181A-3	Sequence 3, Appli,	Sequence 188617,
106	8	US-10-136-728-50	Sequence 50, Appli	Sequence 107891,
107	8	US-10-437-963-107716	Sequence 107716,	Sequence 107829,
108	8	US-10-437-963-107675	Sequence 107675,	Sequence 107844,
109	8	US-10-437-963-155833	Sequence 155833,	Sequence 107862,
110	8	US-10-437-963-138198	Sequence 138198,	Sequence 150509,
111	8	US-10-732-923-18652	Sequence 18652,	Sequence 188720,
112	8	US-10-437-963-124129	Sequence 124129,	Sequence 194013,
113	8	US-10-437-963-107895	Sequence 107895,	Sequence 107741,
114	8	US-10-437-963-151020	Sequence 151020,	Sequence 130234,
115	8	US-10-437-963-188661	Sequence 188661,	Sequence 188689,
116	8	US-10-437-963-154109	Sequence 154109,	Sequence 107783,
117	8	US-10-437-963-107845	Sequence 107845,	Sequence 151015,
118	8	US-10-437-963-188745	Sequence 188745,	Sequence 107777,
119	8	US-10-437-963-159102	Sequence 159102,	Sequence 107828,
120	8	US-10-437-963-138204	Sequence 138204,	Sequence 150230,
121	8	US-10-437-963-107895	Sequence 107895,	Sequence 188689,
122	8	US-10-437-963-180028	Sequence 180028,	Sequence 107784,
123	8	US-10-437-963-151409	Sequence 151409,	Sequence 188695,
124	8	US-10-437-963-107645	Sequence 107645,	Sequence 107638,
125	8	US-10-437-963-146158	Sequence 146158,	Sequence 156513,
126	8	US-10-437-963-146158	Sequence 146158,	Sequence 158749,
127	8	US-10-437-963-146171	Sequence 146171,	Sequence 107720,
128	8	US-10-437-963-183943	Sequence 183943,	Sequence 107783,
129	8	US-10-437-963-195091	Sequence 195091,	Sequence 15105,
130	8	US-10-437-963-194012	Sequence 194012,	Sequence 156437,
131	8	US-10-437-963-146158	Sequence 146158,	Sequence 158780,
132	8	US-10-437-963-107894	Sequence 107894,	Sequence 188726,
133	8	US-10-437-963-156480	Sequence 156480,	Sequence 188633,
134	8	US-10-437-963-130259	Sequence 130259,	Sequence 146169,
135	8	US-10-437-963-107733	Sequence 107733,	Sequence 188659,
136	8	US-10-437-963-107632	Sequence 107632,	Sequence 156437,
137	8	US-10-437-963-188664	Sequence 188664,	Sequence 107780,
138	8	US-10-437-963-164013	Sequence 164013,	Sequence 188726,
139	8	US-10-437-963-156480	Sequence 156480,	Sequence 188924,
140	8	US-10-437-963-130259	Sequence 130259,	Sequence 151019,
141	8	US-10-437-963-164004	Sequence 164004,	Sequence 164016,
142	8	US-10-437-963-188625	Sequence 188625,	Sequence 188721,
143	8	US-10-437-963-188731	Sequence 188731,	Sequence 126, App
144	8	US-10-437-963-164011	Sequence 164011,	Sequence 1, App1
145	8	US-10-437-963-107679	Sequence 107679,	Sequence 2138, App
146	8	US-10-437-963-188684	Sequence 188684,	Sequence 266, App
147	8	US-10-437-963-188625	Sequence 188625,	Sequence 228253,
148	8	US-10-437-963-194957	Sequence 194957,	Sequence 204921,
149	8	US-10-437-963-188625	Sequence 188625,	Sequence 17635,
150	8	US-10-437-963-188655	Sequence 188655,	Sequence 324204,
151	8	US-10-437-963-107822	Sequence 107822,	Sequence 180080,
152	8	US-10-437-963-188625	Sequence 188625,	Sequence 149839,
153	8	US-10-437-963-188625	Sequence 188625,	Sequence 149839,
154	8	US-10-437-963-188625	Sequence 188625,	Sequence 149839,
155	8	US-10-437-963-188625	Sequence 188625,	Sequence 149839,
156	8	US-10-437-963-155453	Sequence 155453,	Sequence 149839,
157	8	US-10-437-963-107816	Sequence 107816,	Sequence 149839,

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OM protein - protein search, using sw model

Run on: July 9, 2005, 06:46:03 ; Search time 28.807 Seconds

(without alignments)

1282.720 Million cell updates/sec

Title: US-09-776-865-4

Perfect score: 495

Sequence: 1 MKSPVSDLAPSDEEESDRT.....LFAKGGVQNWAISDHGCHRN 495

Scoring table: Oligo

Gapext 60.0 , Gapext 60.0

Searched: 513545 seqs, 74649064 residues

Word size : 0

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Issued Patents At:\*

1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep \*

2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep \*

3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep \*

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5: /cgn2\_6/ptodata/1/iaa/pept COMB.pep:\*

6: /cgn2\_6/ptodata/1/iaa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No. Score Query Match Length DB ID Description

Result No.	Score	Query	Match	Length	DB	ID	Description
1	495	100.0	495	4	US-09-359-167-4	Sequence 4, Appli	
2	61	12.3	495	4	US-09-359-167-2	Sequence 2, Appli	
3	61	12.3	495	4	US-09-359-181A-7	Sequence 7, Appli	
4	61	12.3	536	4	US-09-359-167-8	Sequence 8, Appli	
5	61	12.3	585	4	US-09-949-016-7705	Sequence 7705, Appli	
6	14	2.8	495	4	US-09-159-167-10	Sequence 10, Appli	
7	14	2.8	495	4	US-09-359-167-12	Sequence 12, Appli	
8	12	2.4	436	4	US-09-949-016-11448	Sequence 11448, Appli	
9	12	2.4	470	2	US-09-724-394A-10	Sequence 10, Appli	
10	11	2.2	578	4	US-09-740-041-4	Sequence 4, Appli	
11	11	2.2	582	4	US-09-915-81A-4	Sequence 4, Appli	
12	10	2.0	465	4	US-09-151-181A-8	Sequence 8, Appli	
13	8	1.6	140	4	US-09-270-167-33069	Sequence 33069, Appli	
14	8	1.6	140	4	US-09-270-167-18286	Sequence 48286, Appli	
15	8	1.6	171	4	US-09-902-540-15679	Sequence 15679, Appli	
16	8	1.6	234	4	US-09-252-991A-28420	Sequence 28420, Appli	
17	8	1.6	367	4	US-09-328-052-6126	Sequence 6126, Appli	
18	8	1.6	380	4	US-09-949-016-7053	Sequence 7053, Appli	
19	8	1.6	401	4	US-09-328-052-6362	Sequence 6962, Appli	
20	8	1.6	497	4	US-09-949-016-6616	Sequence 6616, Appli	
21	8	1.6	560	1	US-08-647-484-2	Sequence 2, Appli	
22	8	1.6	560	1	US-08-647-481-2	Sequence 2, Appli	
23	8	1.6	560	1	US-08-430-333A-2	Sequence 2, Appli	
24	8	1.6	560	2	US-08-805-118-4	Sequence 4, Appli	
25	8	1.6	560	3	US-09-391-958-4	Sequence 4, Appli	
26	8	1.6	560	4	US-09-915-181A-5	Sequence 5, Appli	
27	8	1.6	560	5	PCT-US96-05792-2	Sequence 2, Appli	

28	8	1.6	567	4	US-09-949-016-11354	Sequence 11354, Appli
29	8	1.6	589	4	US-09-740-041-2	Sequence 2, Appli
30	8	1.6	850	4	US-09-915-181A-3	Sequence 6074, Appli
31	7	1.4	48	4	US-09-270-767-60724	Sequence 8118, Appli
32	7	1.4	91	4	US-09-543-681A-8118	Sequence 22842, Appli
33	7	1.4	93	4	US-09-248-796A-22842	Sequence 16613, Appli
34	7	1.4	96	4	US-09-252-991A-16613	Sequence 2592, Appli
35	7	1.4	102	4	US-09-710-279-2592	Sequence 14320, Appli
36	7	1.4	110	4	US-09-248-796A-14320	Sequence 19987, Appli
37	7	1.4	122	3	US-09-134-001C-487	Sequence 25112, Appli
38	7	1.4	135	4	US-09-252-991A-25112	Sequence 5, Appli
39	7	1.4	140	1	US-08-133-347-5	Sequence 7180, Appli
40	7	1.4	142	4	US-09-99-016-7180	Sequence 267, Appli
41	7	1.4	157	4	US-09-673-395A-267	Sequence 44201, Appli
42	7	1.4	157	4	US-09-270-167-44201	Sequence 10851, Appli
43	7	1.4	163	4	US-09-270-767-32926	Sequence 32926, Appli
44	7	1.4	177	4	US-09-489-039A-11522	Sequence 11522, Appli
45	7	1.4	187	3	US-09-194-185-1	Sequence 1, Appli
46	7	1.4	195	4	US-09-949-016-10851	Sequence 10851, Appli
47	7	1.4	204	4	US-09-549-831-6	Sequence 6, Appli
48	7	1.4	212	4	US-09-934-911-10	Sequence 10, Appli
49	7	1.4	212	4	US-09-934-868-20	Sequence 20, Appli
50	7	1.4	212	4	US-09-248-796A-20354	Sequence 20354, Appli
51	7	1.4	212	4	US-10-321-210-10	Sequence 10, Appli
52	7	1.4	212	4	US-10-320-874-10	Sequence 10, Appli
53	7	1.4	225	4	US-09-252-991A-29348	Sequence 29348, Appli
54	7	1.4	225	4	US-09-270-167-45231	Sequence 45231, Appli
55	7	1.4	228	4	US-09-540-236-798	Sequence 2798, Appli
56	7	1.4	279	3	US-08-549-515-7	Sequence 7, Appli
57	7	1.4	282	4	US-09-583-11-380	Sequence 4800, Appli
58	7	1.4	287	4	US-09-107-333-1120	Sequence 4120, Appli
59	7	1.4	291	4	US-09-252-991A-28572	Sequence 28572, Appli
60	7	1.4	297	4	US-09-52-911A-24412	Sequence 24412, Appli
61	7	1.4	301	4	US-09-902-540-15018	Sequence 15018, Appli
62	7	1.4	306	4	US-09-134-000C-4155	Sequence 4155, Appli
63	7	1.4	307	4	US-09-522-714-16	Sequence 16, Appli
64	7	1.4	307	4	US-09-489-039A-10116	Sequence 10116, Appli
65	7	1.4	308	4	US-09-583-110-950	Sequence 2950, Appli
66	7	1.4	310	4	US-09-543-681A-6311	Sequence 6311, Appli
67	7	1.4	310	4	US-09-248-796A-17322	Sequence 17322, Appli
68	7	1.4	311	4	US-09-489-039A-9786	Sequence 9786, Appli
69	7	1.4	311	4	US-09-107-43-3357	Sequence 3357, Appli
70	7	1.4	313	4	US-09-949-016-6679	Sequence 6679, Appli
71	7	1.4	326	4	US-09-949-016-1456	Sequence 11456, Appli
72	7	1.4	347	4	US-09-949-016-1456	Sequence 26643, Appli
73	7	1.4	348	4	US-09-52-911A-16643	Sequence 31, Appli
74	7	1.4	351	4	US-08-843-530B-31	Sequence 28, Appli
75	7	1.4	351	4	US-09-636-728-28	Sequence 26034, Appli
76	7	1.4	362	4	US-09-248-796A-16034	Sequence 28, Appli
77	7	1.4	381	4	US-09-721-870-28	Sequence 2, Appli
78	7	1.4	431	1	US-08-311-023-2	Sequence 2, Appli
79	7	1.4	441	4	US-09-134-000C-6501	Sequence 4501, Appli
80	7	1.4	451	4	US-09-578-063-43	Sequence 43, Appli
81	7	1.4	460	4	US-09-252-991A-28387	Sequence 28387, Appli
82	7	1.4	465	4	US-09-041-132A-8	Sequence 18003, Appli
83	7	1.4	467	2	US-08-805-118-3	Sequence 3, Appli
84	7	1.4	467	3	US-09-391-958-3	Sequence 3, Appli
85	7	1.4	469	4	US-09-39A-10553	Sequence 16043, Appli
86	7	1.4	469	4	US-09-248-796A-14616	Sequence 14616, Appli
87	7	1.4	470	4	US-09-578-063-69	Sequence 69, Appli
88	7	1.4	473	4	US-09-252-991A-15789	Sequence 28387, Appli
89	7	1.4	480	2	US-08-724-394A-9	Sequence 9, Appli
90	7	1.4	488	3	US-09-099-053-2	Sequence 2, Appli
91	7	1.4	491	4	US-09-252-991A-19014	Sequence 19014, Appli
92	7	1.4	503	4	US-09-489-039A-10722	Sequence 10722, Appli
93	7	1.4	512	4	US-09-902-540-15789	Sequence 15789, Appli
94	7	1.4	540	4	US-09-252-991A-22555	Sequence 22555, Appli
95	7	1.4	563	4	US-09-915-181A-6	Sequence 6, Appli
96	7	1.4	574	4	US-09-248-796A-16849	Sequence 16849, Appli
97	7	1.4	576	3	US-08-864-185-1	Sequence 1, Appli
98	7	1.4	579	4	US-09-252-991A-29372	Sequence 29372, Appli
99	7	1.4	599	4	US-09-949-016-7256	Sequence 7256, Appli
100	7	1.4	651	4	US-09-0489-039A-7892	Sequence 7892, Appli

101	1.4	663	1	US-08-441-139-7	Sequence 7, Appli	Sequence 22061, A	
102	7	678	1	US-08-282-141-2	Sequence 2, Appli	Sequence 6579, Ap	
103	7	678	1	US-08-435-134-2	Sequence 2, Appli	Sequence 165, App	
104	7	1.4	678	1	US-08-135-136-2	Sequence 2, Appli	Sequence 4904, Ap
105	7	1.4	678	2	US-08-438-163-2	Sequence 2, Appli	Sequence 14123, A
106	7	1.4	678	2	US-08-438-164-2	Sequence 2, Appli	Sequence 10196, A
107	7	1.4	678	3	US-08-438-162-2	Sequence 2, Appli	Sequence 6964, Ap
108	7	1.4	678	3	US-08-628-147-2	Sequence 2, Appli	Sequence 21501, A
109	7	1.4	678	3	US-08-402-153-2	Sequence 2, Appli	Sequence 27413, A
110	7	1.4	678	3	US-08-443-166B-2	Sequence 2, Appli	Sequence 4574, Ap
111	7	1.4	722	4	US-08-252-191A-17407	Sequence 2, Appli	Sequence 7165, Ap
112	7	1.4	755	4	US-08-642-134-5	Sequence 5, Appli	Sequence 40827, A
113	7	1.4	832	4	US-09-252-17267	Sequence 17267, A	Sequence 56043, A
114	7	1.4	834	4	US-09-404-967C-5	Sequence 5, Appli	Sequence 97, Appli
115	7	1.4	850	4	US-09-328-152-7660	Sequence 766, Ap	Sequence 169, App
116	7	1.4	859	1	PCT-US95-580-2	Sequence 2, Appli	Sequence 12274, A
117	7	1.4	859	5	PCT-US95-02792-2	Sequence 2, Appli	Sequence 13864, A
118	7	1.4	877	1	US-08-430-125A-4	Sequence 4, Appli	Sequence 21, Appli
119	7	1.4	891	4	US-09-949-016-7798	Sequence 7798, Ap	Sequence 9235, Ap
120	7	1.4	937	4	US-09-949-016-8286	Sequence 8286, Ap	Sequence 10094, A
121	7	1.4	947	4	US-09-152-091A-9359	Sequence 29359, A	Sequence 11231, A
122	7	1.4	949	4	US-09-198-052-778	Sequence 2, Appli	Sequence 11144, A
123	7	1.4	967	4	US-09-438-185A-453	Sequence 453, Appli	Sequence 11503, A
124	7	1.4	1046	4	US-09-252-091A-16902	Sequence 16902, A	Sequence 11942, A
125	7	1.4	1055	4	US-09-404-967C-2	Sequence 2, Appli	Sequence 12092, A
126	7	1.4	1075	4	US-09-404-967C-4	Sequence 4, Appli	Sequence 12220, A
127	7	1.4	1121	4	US-09-949-016-11048	Sequence 11048, A	Sequence 1160, Ap
128	7	1.4	1169	1	US-08-313-168-4	Sequence 4, Appli	Sequence 5353, Ap
129	7	1.4	1255	4	US-09-902-540-12628	Sequence 12628, A	Sequence 399, App
130	7	1.4	1309	4	US-09-975-113A-10	Sequence 10, Appli	Sequence 6720, Ap
131	7	1.4	1318	4	US-10-237-551-17	Sequence 197, Ap	Sequence 27193, A
132	7	1.4	1341	4	US-09-252-991A-26785	Sequence 26785, A	Sequence 8805, Ap
133	7	1.4	1374	4	US-09-900-125B-2	Sequence 2, Appli	Sequence 4256, Ap
134	7	1.4	1865	1	US-08-588-185B-2	Sequence 2, Appli	Sequence 2805, Ap
135	7	1.4	1865	1	US-08-971-988-2	Sequence 12628, A	Sequence 56738, A
136	7	1.4	1865	4	US-09-949-016-6069	Sequence 10, Appli	Sequence 4651, Ap
137	7	1.4	3647	4	US-09-949-016-10932	Sequence 10332, A	Sequence 10406, A
138	7	1.4	15281	2	US-08-471-119A-2	Sequence 2, Appli	Sequence 25200, A
139	6	1.2	5	PCT-US92-0433A-2	Sequence 7, Appli	Sequence 9870, Ap	
140	6	1.2	10	4	US-09-653-165B-11	Sequence 2, Appli	Sequence 12, Appli
141	6	1.2	10	4	US-09-191-593-41	Sequence 41, Appli	Sequence 19059, A
142	6	1.2	12	4	US-10-118-175A-18	Sequence 18, Appli	Sequence 15960, A
143	6	1.2	13	4	US-09-190-176B-2	Sequence 2, Appli	Sequence 6119, Ap
144	6	1.2	16	2	US-08-642-406A-12	Sequence 12, Appli	Sequence 39428, A
145	6	1.2	16	3	US-09-199-534-12	Sequence 12, Appli	Sequence 54645, A
146	6	1.2	16	4	US-09-743-12	Sequence 12, Appli	Sequence 31360, A
147	6	1.2	20	4	US-08-744-419-10	Sequence 10, Appli	Sequence 47177, A
148	6	1.2	24	2	US-09-047-126A-15	Sequence 16, Appli	Sequence 7014, Ap
149	6	1.2	25	4	US-09-270-767-59886	Sequence 59886, A	Sequence 4431, Ap
150	6	1.2	40	4	US-09-091-097-53	Sequence 53, Appli	Sequence 8118, Ap
151	6	1.2	34	1	US-07-745-206A-5	Sequence 5, Appli	Sequence 9597, Ap
152	6	1.2	41	4	US-09-199-534-12	Sequence 12, Appli	Sequence 40845, A
153	6	1.2	41	4	US-08-223-105C-50	Sequence 50, Appli	Sequence 56061, A
154	6	1.2	34	2	US-08-311-363-5	Sequence 18, Appli	Sequence 41, Appli
155	6	1.2	36	2	US-08-846-162-59	Sequence 59, Appli	Sequence 5398, A
156	6	1.2	44	4	US-09-602-177A-12	Sequence 12, Appli	Sequence 25454, A
157	6	1.2	41	4	US-09-740-767-36936	Sequence 5, Appli	Sequence 6555, Ap
158	6	1.2	34	1	US-08-443A-50	Sequence 50, Appli	Sequence 4280, Ap
159	6	1.2	42	4	US-09-270-167-5153	Sequence 52153, A	Sequence 4993, Ap
160	6	1.2	51	4	US-09-270-167-57646	Sequence 998, App	Sequence 61624, A
161	6	1.2	56	4	US-09-621-976-6964	Sequence 57646, A	Sequence 7262, Ap
162	6	1.2	59	4	US-09-205-58-257	Sequence 257, Appli	Sequence 9, Appli
163	6	1.2	45	3	US-09-018-335-39	Sequence 39, Appli	Sequence 4281, A
164	6	1.2	45	4	US-09-912-062-39	Sequence 39, Appli	Sequence 4992, Ap
165	6	1.2	50	3	PCT-US95-056A-1	Sequence 1, Appli	Sequence 4993, Ap
166	6	1.2	51	4	US-09-471-776-398	Sequence 998, App	Sequence 61624, A
167	6	1.2	56	4	US-09-489-039A-10796	Sequence 47143, A	Sequence 7262, Ap
168	6	1.2	59	4	US-09-621-976-6964	Sequence 57646, A	Sequence 5398, A
169	6	1.2	59	4	US-09-248-196A-21439	Sequence 24784, A	Sequence 44149, A
170	6	1.2	62	4	US-09-248-196A-21439	Sequence 21439, A	Sequence 5202, Ap
171	6	1.2	62	4	US-09-248-196A-25193	Sequence 25193, A	Sequence 5202, Ap
172	6	1.2	64	4	US-09-248-196A-26590	Sequence 26590, A	Sequence 22545, A



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102	7	1.4	76	ABP08020	Methylolomo	1.4	207	
103	7	1.4	91	ABP07883	Aaa22300	1.4	207	
104	7	1.4	96	ABO67867	Methylolomo	1.4	207	
105	7	1.4	99	AAU30972	Pseudomon	1.4	207	
106	7	1.4	102	AAQ82749	Novel hum	1.4	207	
107	7	1.4	103	ADA54545	S. epider	1.4	207	
108	7	1.4	107	ABP35197	Human pro	1.4	207	
109	7	1.4	110	AAU91463	Abp31460	Human imm	1.4	207
110	7	1.4	115	ABP31680	Abp31660	Human ORF	1.4	207
111	7	1.4	115	ABR66927	Abp08133	Bacterial	1.4	207
112	7	1.4	115	ADR66927	Abp08133	Pseudomon	1.4	207
113	7	1.4	122	ABP40142	Abp08133	Novel hum	1.4	207
114	7	1.4	122	ABP07186	Abp08133	Staphyloc	1.4	207
121	7	1.4	126	ABU49557	Abp08133	Human tra	1.4	207
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126	7	1.4	136	ADM04743	Abp08133	Pseudomon	1.4	207
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128	7	1.4	145	AAW94926	Abp08133	T cell ac	1.4	207
129	7	1.4	146	ADS17938	Abp08133	Human phe	1.4	207
130	7	1.4	146	ADM19346	Abp08133	Coccidioidi	1.4	207
131	7	1.4	147	AAU43546	Abp08133	Human sec	1.4	207
132	7	1.4	147	AAU19399	AAU91939	Human pol	1.4	207
133	7	1.4	147	AAU81555	AAU81555	Novel hum	1.4	207
134	7	1.4	147	ADU54810	Abp08133	Novel cen	1.4	207
135	7	1.4	155	ADM24567	Abp08133	Novel hum	1.4	207
136	7	1.4	155	ABP53231	Abp08133	Abd24567	1.4	207
137	7	1.4	155	ABAB24501	Abp08133	Human hum	1.4	207
138	7	1.4	155	AAU74756	Abp08133	Abd24501	1.4	207
139	7	1.4	157	AAU80667	Abp08133	Novel hum	1.4	207
140	7	1.4	161	ABU20231	Abp08133	Abd24501	1.4	207
141	7	1.4	163	AAU13183	Abp08133	Abd24501	1.4	207
142	7	1.4	166	ABO65005	Abp08133	Abd24501	1.4	207
143	7	1.4	171	AAU13182	Abp08133	Abd24501	1.4	207
144	7	1.4	172	AAU13182	Abp08133	Abd24501	1.4	207
145	7	1.4	172	ABP9987	Abp08133	Abd24501	1.4	207
146	7	1.4	173	ADM26716	Abp08133	Abd24501	1.4	207
147	7	1.4	175	ABP78104	Abp08133	Abd24501	1.4	207
148	7	1.4	177	AAU91940	Abp08133	Abd24501	1.4	207
149	7	1.4	185	AAU90594	Abp08133	Abd24501	1.4	207
150	7	1.4	185	ADC9950	Abp08133	Abd24501	1.4	207
151	7	1.4	186	AAU90616	Abp08133	Abd24501	1.4	207
152	7	1.4	187	AAU91072	Abp08133	Abd24501	1.4	207
153	7	1.4	187	AAU91019	Abp08133	Abd24501	1.4	207
154	7	1.4	188	AAU90753	Abp08133	Abd24501	1.4	207
155	7	1.4	188	AAU90732	Abp08133	Abd24501	1.4	207
156	7	1.4	192	AAU72437	Abp08133	Abd24501	1.4	207
157	7	1.4	192	AAU72437	Abp08133	Abd24501	1.4	207
158	7	1.4	192	AAU72437	Abp08133	Abd24501	1.4	207
159	7	1.4	192	AAU72437	Abp08133	Abd24501	1.4	207
160	7	1.4	193	AAU72437	Abp08133	Abd24501	1.4	207
161	7	1.4	193	AAU72437	Abp08133	Abd24501	1.4	207
162	7	1.4	194	AAU72437	Abp08133	Abd24501	1.4	207
163	7	1.4	194	AAU72437	Abp08133	Abd24501	1.4	207
164	7	1.4	194	AAU72437	Abp08133	Abd24501	1.4	207
165	7	1.4	194	AAU72437	Abp08133	Abd24501	1.4	207
166	7	1.4	194	AAU72437	Abp08133	Abd24501	1.4	207
167	7	1.4	194	AAU72437	Abp08133	Abd24501	1.4	207
168	7	1.4	194	AAU72437	Abp08133	Abd24501	1.4	207
169	7	1.4	194	AAU72437	Abp08133	Abd24501	1.4	207
170	7	1.4	194	AAU72437	Abp08133	Abd24501	1.4	207
171	7	1.4	194	AAU72437	Abp08133	Abd24501	1.4	207

99	44	ABU01493	S. pneumo	Aar05800	Tilapia (	1.4	7	
100	7	1.4	76	AAU65452	Propionib	1.4	207	
101	7	1.4	76	ABM61971	Propionib	1.4	207	
102	7	1.4	81	ABP08020	Human ORF	1.4	207	
103	7	1.4	91	ADP07883	Bacterial	1.4	207	
104	7	1.4	96	ABO67867	Pseudomon	1.4	207	
105	7	1.4	99	AAU10972	Novel hum	1.4	207	
106	7	1.4	102	AAQ82749	S. epider	1.4	207	
107	7	1.4	103	ADA54545	Ada54545	Human pro	1.4	207
108	7	1.4	107	ABP35197	Abp08133	Human pro	1.4	207
109	7	1.4	110	AAU91463	Abp08133	Human imm	1.4	207
110	7	1.4	115	ABP31680	Abp08133	Human ORF	1.4	207
111	7	1.4	115	ABR66927	Abp08133	Human pro	1.4	207
112	7	1.4	115	ADR66927	Abp08133	Human pro	1.4	207
113	7	1.4	122	ABP40142	Abp08133	Staphyloc	1.4	207
114	7	1.4	122	ABP07186	Abp08133	Staphyloc	1.4	207
121	7	1.4	126	ABU49557	Abp08133	Protein e	1.4	207
122	7	1.4	132	AAB59519	Abp08133	Protein e	1.4	207
123	7	1.4	132	ADM25718	Abp08133	Protein e	1.4	207
124	7	1.4	133	ABB68834	Abp08133	Protein e	1.4	207
125	7	1.4	135	ABO76366	Abp08133	Protein e	1.4	207
126	7	1.4	136	ADM04743	Abp08133	Protein e	1.4	207
127	7	1.4	136	ADQ96342	Abp08133	Protein e	1.4	207
128	7	1.4	145	AAW94926	Abp08133	Protein e	1.4	207
129	7	1.4	145	ADM25718	Abp08133	Protein e	1.4	207
130	7	1.4	146	ABR66927	Abp08133	Protein e	1.4	207
131	7	1.4	147	AAU19399	AAU19399	Novel hum	1.4	207
132	7	1.4	147	AAU81555	AAU81555	Novel hum	1.4	207
133	7	1.4	147	ADU54810	Abp08133	Novel hum	1.4	207
134	7	1.4	147	ADM24567	Abp08133	Novel hum	1.4	207
135	7	1.4	155	ABP53231	Abp08133	Abd24567	1.4	207
136	7	1.4	155	ABAB24501	Abp08133	Abd24567	1.4	207
137	7	1.4	155	AAU74756	Abp08133	Abd24567	1.4	207
138	7	1.4	157	AAU80667	Abp08133	Abd24567	1.4	207
139	7	1.4	157	ABU20231	Abp08133	Abd24567	1.4	207
140	7	1.4	161	AAU13183	Abp08133	Abd24567	1.4	207
141	7	1.4	163	ADM19400	Abp08133	Abd24567	1.4	207
142	7	1.4	166	ABO65005	Abp08133	Abd24567	1.4	207
143	7	1.4	171	AAU13182	Abp08133	Abd24567	1.4	207
144	7	1.4	172	AAU13182	Abp08133	Abd24567	1.4	207
145	7	1.4	172	ABP9987	Abp08133	Abd24567	1.4	207
146	7	1.4	173	ADM26716	Abp08133	Abd24567	1.4	207
147	7	1.4	175	ABP78104	Abp08133	Abd24567	1.4	207
148	7	1.4	177	AAU91940	Abp08133	Abd24567	1.4	207
149	7	1.4	177	AAU90594	Abp08133	Abd24567	1.4	207
150	7	1.4	186	AAU90616	Abp08133	Abd24567	1.4	207
151	7	1.4	187	AAU91072	Abp08133	Abd24567	1.4	207
152	7	1.4	187	AAU71372	Abp08133	Abd24567	1.4	207
153	7	1.4	187	AAU91019	Abp08133	Abd24567	1.4	207
154	7	1.4	188	AAU90753	Abp08133	Abd24567	1.4	207
155	7	1.4	188	AAU90732	Abp08133	Abd24567	1.4	207
156	7	1.4	192	AAU72437	Abp08133	Abd24567	1.4	207
157	7	1.4	200	AAU72437	Abp08133	Abd24567	1.4	207
158	7	1.4	201	AAU72437	Abp08133	Abd24567	1.4	207
159	7	1.4	202	AAU72437	Abp08133	Abd24567	1.4	207
160	7	1.4	203	AAU72437	Abp08133	Abd24567	1.4	207
161	7	1.4	203	AAU72437	Abp08133	Abd24567	1.4	207
162	7	1.4	204	AAU72437	Abp08133	Abd24567	1.4	207
163	7	1.4	204	AAU72437	Abp08133	Abd24567	1.4	207
164	7	1.4	204	AAU72437	Abp08133	Abd24567	1.4	207
165	7	1.4	204	AAU72437	Abp08133	Abd24567	1.4	207
166	7	1.4	204	AAU72437	Abp08133	Abd24567	1.4	207
167	7	1.4	204	AAU72437	Abp08133	Abd24567	1.4	207
168	7	1.4</td						

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 9, 2005, 06:30:47 ; Search time 119.573 Seconds  
 (without alignments)

2295.451 Million cell updates/sec

Title: US-09-776-865-2

Perfect score: 536

Sequence: 1. MAGAGMTPPRVPQPARPGFP.....LFAKGEVQNWLNDHGHHRH 536

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1612378 seqs, 512079187 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : UniProt 03:\*

1: uniprot\_sprot:  
 2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No. Score Query Match Length DB ID Description

Result No.	Score	Query	Match	Length	DB	ID	Description
1	495	92.4	495	1	S175_HUMAN	Q9mz2	homo sapien
2	61	11.4	495	1	S175_SHEEP	Q9mz1	ovis aries
3	34	6.3	495	1	S175_MOUSE	Q8bn12	mus musculu
4	1	2.1	157	2	S96KL7	Q6k117	homo sapien
5	11	2.1	465	1	NPT1_HUMAN	Q14916	homo sapien
6	11	2.1	467	2	S9H531	Q9h531	homo sapien
7	11	2.1	582	2	S9P2U8	Q9P2U8	homo sapien
8	11	2.1	582	2	S920B7	Q920B7	mus musculu
9	11	2.1	582	2	S9B1E7	Q9B1E7	mus musculu
10	11	2.1	582	2	S9J1J2	Q9J1J2	rattus norvegicus
11	10	1.9	172	2	S7PWK3	Q7Pwk3	anopheles gambiae
12	10	1.9	363	2	S9BWS1	Q8Bws1	mus musculu
13	10	1.9	436	1	NPT3_HUMAN	Q00634	homo sapien
14	10	1.9	447	2	S9VCX8	Q8vcx8	mus musculu
15	10	1.9	466	2	S96LH1	Q96Lh1	homo sapien
16	10	1.9	535	2	S9Pwk4	Q7Pwk4	anopheles gambiae
17	10	1.9	544	1	T9T3_CABEL	Q10046	caenorhabditis elegans
18	10	1.9	573	2	S09932	Q09932	caenorhabditis elegans
19	9	1.7	69	2	S91Y99	Q91Y99	mus musculu
20	9	1.7	127	2	S71118	Q71118	trichoplax
21	9	1.7	286	2	S7PRG4	Q7Prg4	anopheles gambiae
22	9	1.7	390	2	S921B2	Q921B2	mus musculu
23	9	1.7	465	1	NPT1_MOUSE	Q61933	mus musculu
24	9	1.7	465	1	NPT1_RAT	Q62275	rattus norvegicus
25	9	1.7	465	2	S9K3H3	Q8k3h3	rattus norvegicus
26	9	1.7	465	2	S91WV5	Q91Wv5	mus musculu
27	9	1.7	465	2	S9AZ46	Q6az46	rattus norvegicus
28	9	1.7	469	2	S9CJH8	Q8CJh8	rattus norvegicus
29	9	1.7	475	2	S9AZ69	Q6az69	drosophila melanogaster
30	9	1.7	497	2	S8MRP7	Q8mrp7	drosophila melanogaster
31	9	1.7	498	2	S9CJH9	Q8CJh9	rattus norvegicus

32	9	1.7	083248	treponema	p
33	8	1.5	Q78377	neurospora	circinelloid
34	8	1.5	Q9LRG3	chlorrella	v
35	8	1.5	Q9B615	mus musculu	
36	8	1.5	Q99909	potamotrygo	
37	8	1.5	Q97CJ3	thermoplasm	
38	8	1.5	Q9205	salmonella	
39	8	1.5	Q21438	caenorhabditis	
40	8	1.5	Q72Kc7	thermus	thermophilic
41	8	1.5	Q53550	mycobacterium	
42	8	1.5	Q7twc6	mycobacterium	
43	8	1.5	Q7TWC6	mycobacterium	
44	8	1.5	Q674M9	tritaleurodes	
45	8	1.5	Q7Q579	anopheles	gambiae
46	8	1.5	Q402	Q7TQH3	caenorhabditis
47	8	1.5	Q6571	homo sapien	
48	8	1.5	Q7Y7Z7	drosophila	
49	8	1.5	Q8ZZR7	pyrococcus	
50	8	1.5	Q7Q579	anopheles	gambiae
51	8	1.5	Q23514	caenorhabditis	
52	8	1.5	Q9Y2C5	homo sapien	
53	8	1.5	Q6nr28	drosophila	
54	8	1.5	Q7krJ1	homo sapien	
55	8	1.5	Q8VCY5	mus musculu	
56	8	1.5	Q9VDM0	drosophila	
57	8	1.5	Q8JFT2	brachydanio	
58	8	1.5	Q7Q1S5	anopheles	gambiae
59	8	1.5	Q9SY99	arabidopsis	
60	8	1.5	Q7Q580	anopheles	gambiae
61	8	1.5	Q8W033	arabidopsis	
62	8	1.5	Q940H4	arabidopsis	
63	8	1.5	Q8s068	oryza sativa	
64	8	1.5	Q9VYGT	drosophila	
65	8	1.5	Q6PCD0	homo sapien	
66	8	1.5	Q9P2U7	homo sapien	
67	8	1.5	Q62634	rattus norvegicus	
68	8	1.5	Q6INC8	homo sapien	
69	8	1.5	Q8AW47	brachydanio	
70	8	1.5	Q8K1Q1	homo sapien	
71	8	1.5	Q7TSF2	rattus norvegicus	
72	8	1.5	Q8NDX2	homo sapien	
73	8	1.5	Q7Q3R3	anopheles	gambiae
74	8	1.5	Q6BEU8	mus musculu	
75	8	1.5	Q76HP4	seriola	qui
76	8	1.5	Q9U2E0	caenorhabditis	
77	8	1.5	Q9ADL8	polychaeta	
78	8	1.5	Q7SX79	brachydanio	
79	8	1.5	Q6BCK3	figu rubrip	
80	8	1.5	Q6DE12	brachydanio	
81	8	1.5	Q72ZS7	brachydanio	
82	8	1.5	Q7ZT42	brachydanio	
83	8	1.5	Q6BCK4	figu rubrip	
84	8	1.5	Q7ZT45	seriola	qui
85	8	1.5	Q7Q6T9	anopheles	gambiae
86	8	1.5	Q7XTN8	oryza sativa	
87	8	1.5	Q9SMA4	oryza sativa	
88	8	1.5	Q9V701	homo sapien	
89	8	1.5	Q9L036	homo sapien	
90	8	1.5	Q9VAS8	drosophila	
91	8	1.5	Q7ZT13	mus musculu	
92	7	1.3	Q33434	equus cabal	
93	7	1.3	Q33435	equus quagg	
94	7	1.3	Q34493	homo sapien	
95	7	1.3	Q6BAN8	homo sapien	
96	7	1.3	Q88Mk7	pseudomonas	
97	7	1.3	Q61G36	drosophila	
98	7	1.3	Q6H710	oryza sativa	
99	7	1.3	P05689	bos taurus	
100	7	1.3	Q96Pf5	homo sapien	
101	7	1.3	Q711Z3	lactobacillus	
102	7	1.3	Q7U5U3	synchococcus	
103	7	1.3	KRFT_ANAPL	anaeromyces	
104	7	1.3	Q6UXP0	homo sapien	

105	7	99	2	Q924W3	rattus norvegicus	178	7	1.3	Q7ZYV4	odontostethes
106	7	102	2	Q9B219	branchiostoma	179	7	1.3	Q7PWT4	anophales
107	7	103	2	Q84QW1	bacteroides	180	7	1.3	Q65W6	myotis mystacinus
108	7	104	1	Q7ATP THEVO	thermopolasm	181	7	1.3	Q65W6	homo sapiens
109	7	106	2	Q725U9	desulfovibrio	182	7	1.3	Q9d1g2	mus musculus
110	7	107	2	Q13532	saccharomyces	183	7	1.3	Q8YFN3	brucella melitensis
111	7	109	2	Q87TK8	vibrio para	184	7	1.3	Q8G2E0	brucella suis
112	7	114	2	Q32461	actinomadura	185	7	1.3	Q8LN42	coregonus
113	7	115	2	Q37739	felis silvestris	186	7	1.3	Q8M0M2	coregonus
114	7	116	2	Q8HCW7	plecotus aegaeus	187	7	1.3	Q8NbM3	coregonus
115	7	116	2	Q94J6	oryza sativa	188	7	1.3	Q8M0M4	coregonus
116	7	118	2	Q64Q69	bacteroides	189	7	1.3	Q8M0M5	coregonus
117	7	118	2	Q8CRD8	staphylococcus	190	7	1.3	Q8M0M6	coregonus
118	7	124	2	Q9T4W9	argacaria	191	7	1.3	Q8C4W2	mus musculus
119	7	125	1	ND1M ARBLI	lilium	192	7	1.3	Q9Zbb8	chlamydia pneumoniae
120	7	125	2	Q6M0T0	methanococcus	193	7	1.3	Q8M0M3	coregonus
121	7	126	1	ACPS VLBC	vibrio cholerae	194	7	1.3	Q8Q1a9	namestra
122	7	126	2	Q7YTH7	caenorhabditis	195	7	1.3	Q7IA87	namestra
123	7	127	2	Q73ER8	bacillus cereus	196	7	1.3	Q8JTN3	hippoglossus
124	7	127	2	Q7MVK P1G	sus scrofa	197	7	1.3	Q8aG3	siganus guttatus
125	7	129	2	Q8QNQH2	artacia lilia	198	7	1.3	Q823P1	chlamydophila pneumoniae
126	7	129	2	Q7QX3	ectocarpus	199	7	1.3	Q89346	mycobacterium
127	7	129	2	Q8TYH5	methanopyrus	200	7	1.3	Q8J7R7	mycobacterium
128	7	132	2	Q9Y928	aeropyrum pernix	201	7	1.3	Q7M0V7	mycobacterium
129	7	135	2	Q8W1Z8	capsicum	202	7	1.3	Q6MKTU	bdelliothri
130	7	136	2	Q7UX50	rhodopirellus	203	7	1.3	Q6NbV0	drospila
131	7	136	1	YCM2 SCHPO	rhodopirellus	204	7	1.3	Q8NRA3	homo sapiens
132	7	137	2	Q7X8R7	schizosaccharomyces pombe	205	7	1.3	Q79237	thymallus australis
133	7	137	2	Q91L70	giardia lamblia	206	7	1.3	Q98955	thymallus australis
134	7	137	2	Q1NGK7	methanopyrus kishimotoi	207	7	1.3	Q892X5	clostridium
135	7	138	2	Q91TU4	gloeoobacter	208	7	1.3	Q8J2R7	mus musculus
136	7	138	2	Q94WB2	tupaiidae	209	7	1.3	Q9NTR6	homo sapiens
137	7	138	1	Q7UX50	rhodopirellus	210	7	1.3	Q9V8V0	oleaster
138	7	139	2	Q7P179	thymallus	211	7	1.3	Q9FHR1	arabidopsis thaliana
139	7	139	2	Q91L70	oryza sativa	212	7	1.3	Q95566	verasper major
140	7	146	2	Q6QFF8	legionella	213	7	1.3	Q9mgw7	wolinella sphaerica
141	7	148	2	Q91TU4	legionella	214	7	1.3	Q8JINS	cottus kawamurai
142	7	150	2	Q94WD3	prerelectrum	215	7	1.3	Q91282	acanthopagrus
143	7	150	2	Q94WD3	prerelectrum	216	7	1.3	Q4554	pragrus major
144	7	151	2	Q7P179	anopheles gambiae	217	7	1.3	Q95163	dicentra
145	7	151	2	Q48800	legionella	218	7	1.3	Q91283	dicentra
146	7	151	2	Q6QFF8	legionella	219	7	1.3	Q92484	lates californiensis
147	7	151	2	Q6QFG1	legionella	220	7	1.3	Q9mgw7	lates californiensis
148	7	151	2	Q6ORG3	legionella	221	7	1.3	Q91915	odontostethes
149	7	151	2	Q6QFH0	legionella	222	7	1.3	Q94746	oreochromis
150	7	152	2	Q21116	rhizopus stolonifer	223	7	1.3	Q13191	oreochromis
151	7	153	2	Q9KUY1	vibrio cholerae	224	7	1.3	Q9dev3	perca fluviatilis
152	7	154	2	Q1S1E3	neurospora	225	7	1.3	Q91946	pseudosciaenidae
153	7	155	2	Q8W1Z9	capsicum annuum	226	7	1.3	Q91b11	sciadopithecus
154	7	155	2	Q91459	seriola quinquecincta	227	7	1.3	Q91b11	sciadopithecus
155	7	155	2	Q9CCU7	mycobacterium	228	7	1.3	Q99771	sebastes
156	7	156	2	Q9CSW6	rhizopus stolonifer	229	7	1.3	Q909V6	sebastes
157	7	157	2	Q6GKY2	mycobacterium	230	7	1.3	Q909V6	sebastes
158	7	165	2	Q8UDC2	arabidopsis thaliana	231	7	1.3	Q909V6	sebastes
159	7	166	2	Q8LXA6	agrobacteri	232	7	1.3	Q909V6	sebastes
160	7	166	2	Q9UTU7	debaromyces	233	7	1.3	Q909V6	sebastes
161	7	167	2	Q7U595	schizosaccharomyces pombe	234	7	1.3	Q909V6	sebastes
162	7	169	2	Q7NH52	synechococcus	235	7	1.3	Q6QDp2	leporinus
163	7	171	2	Q837C3	rhizopus stolonifer	236	7	1.3	Q7SYG9	leporinus
164	7	171	2	Q9KTH0	enterococcus	237	7	1.3	Q7T1G3	leporinus
165	7	173	2	Q82HKK8	enterococcus	238	7	1.3	Q7T231	leporinus
166	7	174	2	Q9RPS9	streptomyces	239	7	1.3	Q8Btk6	leporinus
167	7	174	2	Q6EGY9	streptomyces	240	7	1.3	Q9rcv9	leporinus
168	7	175	2	Q8EGZ0	rhodopseudomonas	241	7	1.3	Q9CXB8	leporinus
169	7	175	2	Q88ZC1	lactobacillus	242	7	1.3	Q944X3	leporinus
170	7	175	2	Q8EGY7	plecotus australis	243	7	1.3	Q7N6C9	leporinus
171	7	175	2	Q8EGY8	paramaecium	244	7	1.3	Q7H6C9	leporinus
172	7	176	2	Q6EGY9	atsutawakii	245	7	1.3	Q8V7K8	canarypox
173	7	176	2	Q6UWAE1	plecotus australis	246	7	1.3	Q8rtt8	uncultured
174	7	176	2	Q8EGZ1	plecotus australis	247	7	1.3	Q6SPD5	haemophilus
175	7	177	2	Q91077	thunnus albus	248	7	1.3	ATOD_HAETN	haemophilus
176	7	177	2	Q91449	seriola dumetorum	249	7	1.3	OPBB_BACSU	bacillus
177	7	177	2	Q91454	sebastiscus	250	7	1.3	OPCB_BACSU	bacillus

GenCore version 5.1.6  
(c) 1993 - 2005 Compugen Ltd.

**M**rotein - protein search using our model

run on: July 9, 2005, 06:34:43 ; Search time: 27.0339 Seconds  
(without alignments)  
(1907.682 Million Cell updates)

title: US-09-776-8865-2  
perfect score: 536

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searched: 282116 2222 06216763 2222

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maximum DB seq length: 2000000000

post-processing: Listing first 1000 summaries

database : PIB 79:\*

1: **Dir1:=**  
2: **Dir2:=**

3: p113:\*

No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

CONTINENTES

Result No.	Score	Query Match	Length	DB	ID	Description	
		Score	Length	DB	ID		
1	11	2.1	465	2	I39473	Na <sup>+</sup> -dependent phosphatase t	
	2	2.1	467	2	A49916	sodium phosphate t	
	3	10	1.9	544	2	T24633	hypothetical prote
	4	9	1.9	573	2	T23589	hypothetical prote
	5	9	1.7	465	2	S69915	sodium-phosphate t
	6	9	1.7	715	2	H71352	probable sigma fac
	7	8	1.5	250	2	A56572	homeotic protein H
	8	8	1.5	308	2	AG0992	high-affinity bran
	9	8	1.5	308	2	JR0668	high-affinity bran
	10	8	1.5	373	2	C70806	probable fad327 pr
	11	8	1.5	396	2	T23619	hypothetical prote
	12	8	1.5	398	2	G71733	hypothetical prote
	13	8	1.5	465	2	A56410	sodium/phosphate t
	14	8	1.5	479	2	E63613	ATP-dependent RNA
	15	8	1.5	533	2	T04770	aldehyde dehydroge
	16	8	1.5	560	2	I59302	brain specific Na <sup>+</sup>
	17	8	1.5	4128	2	JCS306	protein kinase (EC
	18	7	1.3	33	2	S13863	dihydrofolipoamide d
	19	7	1.3	73	2	A29172	cathepsin B-like c
	20	7	1.3	95	1	KRDKF4	keratin B-4, feath
	21	7	1.3	107	2	S69295	probable membrane
	22	7	1.3	114	2	JCS860	peptidylid e synthas
	23	7	1.3	126	2	F81072	holo- (acyl 1-carrier
	24	7	1.3	133	2	H72476	hypothetical prote
	25	7	1.3	138	2	T40963	very hypothetical prote
	26	7	1.3	151	2	S61384	ICMW protein - Leg
	27	7	1.3	152	2	PT0433	progesterone 11a,1p
	28	7	1.3	153	2	B23330	conserved hypothet
	29	7	1.3	158	2	CB86961	probable tRNA/rRNA

103	7	1.3	T11857	176	7	1.3	G90569
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109	7	1.3	555004	179	7	1.3	T03216
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111	7	1.3	AB0775	180	7	1.3	JC7858
112	7	1.3	322	2	1.3	535	2
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115	7	1.3	QXL1M	182	7	1.3	G95222
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117	7	1.3	323	1	1.3	541	2
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121	7	1.3	58892	185	7	1.3	JC6063
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searched:	1726216 seqs, 386330316 residues	searched:	1726216 seqs, 386330316 residues
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19: /cgn2_6/ptodata/2/pubpaas/US10N_PUBCOMB.pep:*	19: /cgn2_6/ptodata/2/pubpaas/US10N_PUBCOMB.pep:*	20: /cgn2_6/ptodata/2/pubpaas/US11B_PUBCOMB.pep:*	20: /cgn2_6/ptodata/2/pubpaas/US11B_PUBCOMB.pep:*
20: /cgn2_6/ptodata/2/pubpaas/US11C_PUBCOMB.pep:*	20: /cgn2_6/ptodata/2/pubpaas/US11C_PUBCOMB.pep:*	21: /cgn2_6/ptodata/2/pubpaas/US60_PUBCOMB.pep:*	21: /cgn2_6/ptodata/2/pubpaas/US60_PUBCOMB.pep:*
21: /cgn2_6/ptodata/2/pubpaas/US60_PUBCOMB.pep:*	21: /cgn2_6/ptodata/2/pubpaas/US60_PUBCOMB.pep:*	22: /cgn2_6/ptodata/2/pubpaas/US60_PUBCOMB.pep:*	22: /cgn2_6/ptodata/2/pubpaas/US60_PUBCOMB.pep:*
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
SUMMARIES			
ult No.	Score	Match Length	DB ID
1	536	100.0	536 9 US-09-776-865-2
2	536	100.0	536 17 US-10-823-506-8
3	495	92.4	495 16 US-09-915-181A-7
4	495	92.4	495 16 US-10-755-889-588
5	495	92.4	495 17 US-10-823-506-2
6	284	53.0	284 15 US-10-264-049-2477
7	217	40.5	272 15 US-10-264-23-2351
8	180	33.6	194 15 US-10-226-115-1200
9	61	11.4	495 9 US-09-776-865-4
10	61	11.4	495 17 US-10-823-506-10
11	14	2.6	495 17 US-10-823-506-4
12	14	2.6	495 17 US-10-823-506-12
13	11	2.1	467 9 US-09-991-213A-4
14	11	2.1	467 10 US-09-965-522-3
15	11	2.1	467 17 US-10-877-818-3
16	11	2.1	578 14 US-10-389-967-4
17	11	2.1	578 9 US-09-915-181A-4
18	11	2.1	582 16 US-10-734-731-10
19	11	2.1	582 16 US-10-734-731-12
20	11	2.1	582 16 US-10-807-500-10
21	11	2.1	582 16 US-10-807-500-12
22	11	2.1	582 16 US-10-807-500-14
23	11	2.1	582 16 US-10-807-500-16
24	11	2.1	582 16 US-10-807-500-18
25	11	2.1	582 16 US-10-807-500-14
26	10	1.9	544 15 US-10-369-493-5873
27	10	1.9	573 15 US-10-369-493-5871
28	10	1.9	573 15 US-10-369-493-5872
29	9	1.7	465 9 US-09-915-181A-8
30	8	1.5	71 16 US-10-425-115-288336
31	8	1.5	88 16 US-10-425-115-302951
32	8	1.5	114 16 US-10-437-963-128557
33	8	1.5	143 16 US-10-425-115-335986
34	8	1.5	154 16 US-10-767-701-52130
35	8	1.5	232 15 US-10-425-114-43907
36	8	1.5	235 15 US-10-282-122A-156379
37	8	1.5	264 16 US-10-108-260A-3281
38	8	1.5	373 16 US-10-482-706-253
39	8	1.5	384 15 US-10-424-599-183068
40	8	1.5	478 16 US-10-369-493-180400
41	8	1.5	479 15 US-10-369-493-23364
42	8	1.5	512 16 US-10-422-115-335979
43	8	1.5	550 16 US-10-739-930-6619
44	8	1.5	560 9 US-09-991-212A-4
45	8	1.5	560 10 US-09-915-181A-5
46	8	1.5	560 10 US-09-965-522-4
47	8	1.5	560 15 US-10-314-790-5
48	8	1.5	560 16 US-10-734-731-2
49	8	1.5	560 16 US-10-734-731-4
50	8	1.5	560 16 US-10-734-731-6
51	8	1.5	560 16 US-10-734-731-8
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55	8	1.5	560 16 US-10-807-500-8
56	8	1.5	560 17 US-10-499-731-6
57	8	1.5	566 15 US-10-287-226-300
58	8	1.5	566 16 US-10-437-963-112089
59	8	1.5	589 9 US-09-740-041-2
60	8	1.5	589 14 US-10-389-967-2
61	8	1.5	589 18 US-10-499-731-2-8
62	8	1.5	601 18 US-10-499-731-6
63	8	1.5	850 9 US-09-915-181A-3
64	8	1.5	940 16 US-10-437-963-1155813
65	8	1.5	949 17 US-10-733-923-18652
66	8	1.5	950 16 US-10-437-963-107881
67	8	1.5	1031 16 US-10-437-963-107870
68	8	1.3	4128 14 US-10-205-194-1
69	7	1.3	13 15 US-10-469-101-70
70	7	1.3	13 15 US-10-469-101-71
71	7	1.3	13 15 US-10-191-879-31
72	7	1.3	33 10 US-09-983-802-663
73	7	1.3	33 10 US-09-984-490-663
74	7	1.3	33 11 US-09-973-278-444
75	7	1.3	42 15 US-10-424-599-212978
76	7	1.3	77 15 US-10-469-101-70
77	7	1.3	13 15 US-10-191-879-31
78	7	1.3	33 11 US-09-973-278-444
79	7	1.3	44 16 US-10-885-039-126
80	7	1.3	58 16 US-10-425-115-350119
81	7	1.3	59 16 US-10-437-963-204921
82	7	1.3	61 15 US-10-424-599-2186970
83	7	1.3	64 15 US-10-424-599-180080
84	7	1.3	65 16 US-10-437-963-147591
85	7	1.3	66 16 US-10-437-963-147591

85	7	1.3	71	16	US-10-425-115-254514	Sequence 254514,	Sequence 6, Appli
86	7	1.3	71	16	US-10-425-115-3-18386	Sequence 318386,	Sequence 2253, Ap
87	7	1.3	72	16	US-10-437-163-181072,	Sequence 181072,	Sequence 538, App
88	7	1.3	76	15	US-10-424-599-255605	Sequence 255605,	Sequence 538, App
89	7	1.3	77	15	US-10-424-599-168281	Sequence 168281,	Sequence 538, App
90	7	1.3	78	16	US-10-425-115-3-37514	Sequence 357514,	Sequence 3217, A
91	7	1.3	79	10	US-09-764-891-4448	Sequence 4448, Ap	Sequence 1787, A
92	7	1.3	82	9	US-09-864-781-35759	Sequence 35759, A	Sequence 160649,
93	7	1.3	85	16	US-10-437-163-188238	Sequence 188238,	Sequence 1644, A
94	7	1.3	87	15	US-10-424-599-148365	Sequence 148365,	Sequence 1346, Ap
95	7	1.3	88	16	US-10-425-115-253274	Sequence 253274,	Sequence 141, Appli
96	7	1.3	91	16	US-10-425-115-3-10462	Sequence 31062,	Sequence 24, Appli
97	7	1.3	96	15	US-10-424-599-143646	Sequence 241646,	Sequence 103966,
98	7	1.3	97	16	US-10-437-963-11377	Sequence 110377,	Sequence 198853
99	7	1.3	97	16	US-10-425-115-199192	Sequence 199192,	Sequence 6941, A
100	7	1.3	98	16	US-10-437-163-161222	Sequence 161222,	Sequence 141, Ap
101	7	1.3	101	15	US-10-424-599-199724	Sequence 199724,	Sequence 15, App
102	7	1.3	103	15	US-10-094-749-2113	Sequence 2113, Ap	Sequence 10645,
103	7	1.3	103	15	US-10-424-599-143096	Sequence 14096,	Sequence 103966,
104	7	1.3	103	16	US-10-425-115-6181	Sequence 6181,	Sequence 15811,
105	7	1.3	105	16	US-10-425-115-333987	Sequence 333987,	Sequence 62062, A
106	7	1.3	106	14	US-10-083-157-572	Sequence 972, App	Sequence 141, Appli
107	7	1.3	108	16	US-10-425-115-25034	Sequence 253034,	Sequence 31762,
108	7	1.3	110	16	US-10-425-115-246172	Sequence 246172,	Sequence 32619,
109	7	1.3	114	16	US-10-437-963-204470	Sequence 204470,	Sequence 40533, A
110	7	1.3	115	11	US-09-864-48A-126	Sequence 1266, Ap	Sequence 309, App
111	7	1.3	116	16	US-10-437-963-108779	Sequence 108779,	Sequence 2212, Ap
112	7	1.3	116	16	US-10-437-963-195396	Sequence 195396,	Sequence 9239, Ap
113	7	1.3	117	16	US-10-425-115-365789	Sequence 365789,	Sequence 9239, Ap
114	7	1.3	122	14	US-10-312-187-12	Sequence 12, Appli	Sequence 4120, Ap
115	7	1.3	125	16	US-10-425-115-332340	Sequence 332340,	Sequence 494, Ap
116	7	1.3	126	15	US-10-282-122A-77481	Sequence 77481,	Sequence 128, Ap
117	7	1.3	127	15	US-10-424-599-160647	Sequence 160647,	Sequence 104, Appli
118	7	1.3	129	16	US-10-767-701-39962	Sequence 39962,	Sequence 5, Appli
119	7	1.3	133	16	US-10-767-701-49108	Sequence 49108,	Sequence 2, Appli
120	7	1.3	135	10	US-09-764-891-759	Sequence 4759, Ap	Sequence 141, Appli
121	7	1.3	142	16	US-10-437-963-174382	Sequence 174382,	Sequence 4214, Ap
122	7	1.3	143	15	US-10-424-599-213589	Sequence 213589,	Sequence 937, Ap
123	7	1.3	145	16	US-10-437-963-190613	Sequence 190613,	Sequence 16, Appli
124	7	1.3	145	16	US-10-425-115-301015	Sequence 301015,	Sequence 2250, Ap
125	7	1.3	146	16	US-10-437-963-137026	Sequence 137026,	Sequence 4282, Ap
126	7	1.3	151	16	US-10-767-101-33254	Sequence 33254,	Sequence 21705, A
127	7	1.3	151	16	US-10-425-115-206281	Sequence 206281,	Sequence 50442, A
128	7	1.3	152	15	US-10-094-749-1733	Sequence 1723,	Sequence 11380, A
129	7	1.3	153	16	US-10-437-963-174385	Sequence 174385,	Sequence 11380, A
130	7	1.3	153	16	US-10-425-115-301017	Sequence 301017,	Sequence 11545, A
131	7	1.3	155	9	US-09-925-299-831	Sequence 831, App	Sequence 156, App
132	7	1.3	155	10	US-09-925-299-831	Sequence 831, App	Sequence 58828, A
133	7	1.3	155	14	US-09-895-298-127	Sequence 127,	Sequence 164057,
134	7	1.3	155	14	US-10-106-698-5530	Sequence 5530, Ap	Sequence 1209, Ap
135	7	1.3	155	15	US-10-424-599-279690	Sequence 279690,	Sequence 2059, Ap
136	7	1.3	155	16	US-10-885-039-127	Sequence 127,	Sequence 7, Appli
137	7	1.3	158	15	US-10-282-122A-63701	Sequence 63701,	Sequence 4, Appli
138	7	1.3	159	16	US-10-437-963-129515	Sequence 129515,	Sequence 5, Appli
139	7	1.3	163	16	US-10-425-115-209403	Sequence 1,	Sequence 6, Appli
140	7	1.3	163	17	US-10-811-492-1	Sequence 209403,	Sequence 7, Appli
141	7	1.3	163	17	US-10-437-963-190613	Sequence 11037,	Sequence 8, Appli
142	7	1.3	169	15	US-10-425-114-72494	Sequence 72494,	Sequence 9, Appli
143	7	1.3	170	15	US-10-425-114-41569	Sequence 41569,	Sequence 10, Appli
144	7	1.3	171	15	US-10-424-599-143940	Sequence 143940,	Sequence 11, Appli
145	7	1.3	171	16	US-10-425-115-209425	Sequence 209425,	Sequence 12, Appli
146	7	1.3	173	14	US-10-156-761-11037	Sequence 11037,	Sequence 13, Appli
147	7	1.3	174	16	US-10-767-701-34655	Sequence 34655,	Sequence 14, Appli
148	7	1.3	175	15	US-10-425-114-214742	Sequence 214742,	Sequence 15, Appli
149	7	1.3	185	14	US-10-191-879-21	Sequence 21,	Sequence 16, Appli
150	7	1.3	188	15	US-10-424-599-160648	Sequence 160648,	Sequence 17, Appli
151	7	1.3	194	16	US-10-437-963-174369	Sequence 174369,	Sequence 18, Appli
152	7	1.3	195	15	US-10-289-762-444	Sequence 444,	Sequence 19, Appli
153	7	1.3	198	16	US-10-767-701-39961	Sequence 39961,	Sequence 19, Appli
154	7	1.3	199	16	US-10-767-701-36019	Sequence 36019,	Sequence 20, Appli
155	7	1.3	200	14	US-10-017-161-3078	Sequence 1078,	Sequence 21, Appli
156	7	1.3	200	15	US-10-292-798-916	Sequence 916,	Sequence 22, Appli
157	7	1.3	200	15	US-10-424-599-166917	Sequence 166917,	Sequence 23, Appli

GenCore version 5.1.6  
(c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 9, 2005, 06:46:03 ; Search time 31.193 Seconds  
(without alignments)

1282.720 Million Cell updates/sec

Title: US-09-776-865-2

Perfect score: 536

Sequence: 1 MAAGAMTPPRPVQPARGGF.....LPAKGEVQNWNALNDHGHHRH 536

Scoring table: OLIGO

Gapext 60.0 , Gapext 60.0

Searched: 513545 seqs, 74649064 residues

Word size : 0

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Listing first 1000 summaries

Database : Issued Patents AI:\*

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5: /cgn2\_6/prodata/1/iaa/PCTUS.COMB.pep:\*

6: /cgn2\_6/prodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	536	100.0	536	4	US-09-359-167-8	Sequence 8, Appli
2	529	98.7	585	4	US-09-349-016-7705	Sequence 7705, Appli
3	495	92.4	495	4	US-09-359-167-2	Sequence 2, Appli
4	495	92.4	495	4	US-09-915-181A-7	Sequence 7, Appli
5	61	11.4	495	4	US-09-359-167-4	Sequence 4, Appli
6	14	2.6	495	4	US-09-359-167-10	Sequence 10, Appli
7	14	2.6	495	4	US-09-359-167-12	Sequence 12, Appli
8	11	2.1	467	2	US-08-805-18-3	Sequence 3, Appli
9	11	2.1	467	3	US-09-391-958-3	Sequence 3, Appli
10	11	2.1	480	2	US-08-724-594A-9	Sequence 9, Appli
11	11	2.1	578	4	US-09-740-011-4	Sequence 4, Appli
12	11	2.1	582	4	US-09-915-181A-4	Sequence 4, Appli
13	10	1.9	436	4	US-09-949-016-11448	Sequence 11448, Appli
14	10	1.9	470	2	US-08-724-394A-10	Sequence 10, Appli
15	9	1.7	465	4	US-09-915-181A-8	Sequence 8, Appli
16	8	1.5	140	4	US-09-770-167-33069	Sequence 33069, Appli
17	8	1.5	140	4	US-09-270-167-48286	Sequence 48286, Appli
18	8	1.5	173	4	US-09-902-540-10210	Sequence 10210, Appli
19	8	1.5	218	4	US-09-902-540-11754	Sequence 11754, Appli
20	8	1.5	318	4	US-09-902-540-11509	Sequence 11509, Appli
21	8	1.5	380	4	US-09-949-016-7053	Sequence 7053, Appli
22	8	1.5	464	4	US-09-107-532A-5509	Sequence 5509, Appli
23	8	1.5	497	4	US-09-949-016-6616	Sequence 6616, Appli
24	8	1.5	501	4	US-09-252-591A-21596	Sequence 21596, Appli
25	8	1.5	560	1	US-08-647-484-2	Sequence 2, Appli
26	8	1.5	560	1	US-08-647-481-2	Sequence 2, Appli
27	8	1.5	560	1	US-08-430-033A-2	Sequence 2, Appli

Result No.	Score	Query	Match	Length	DB ID	Description
28	8	1.5	560	3	US-09-391-558-4	Sequence 4, Appli
29	8	1.5	560	4	US-09-915-181A-5	Sequence 5, Appli
30	8	1.5	560	5	PCT-US96-05792-2	Sequence 2, Appli
31	8	1.5	560	4	US-09-949-016-11354	Sequence 11354, Appli
32	8	1.5	567	4	US-09-740-041-2	Sequence 2, Appli
33	8	1.5	589	4	US-09-252-991A-26187	Sequence 3, Appli
34	8	1.5	687	4	US-09-915-181A-3	Sequence 3, Appli
35	8	1.5	850	4	US-09-227-357-6633	Sequence 63, Appli
36	7	1.3	33	3	US-09-270-767-60224	Sequence 60224, Appli
37	7	1.3	48	4	US-09-270-767-6063	Sequence 6063, Appli
38	7	1.3	60	4	US-09-621-976-7063	Sequence 987, Appli
39	7	1.3	102	4	US-09-621-976-7063	Sequence 10642, Appli
40	7	1.3	102	4	US-09-279-2592	Sequence 13540, Appli
41	7	1.3	110	4	US-09-248-796A-14320	Sequence 6210, Appli
42	7	1.3	117	4	US-09-270-767-39798	Sequence 39798, Appli
43	7	1.3	117	4	US-09-270-767-55015	Sequence 55015, Appli
44	7	1.3	122	3	US-09-134-0101C-4987	Sequence 4987, Appli
45	7	1.3	122	4	US-09-949-016-10642	Sequence 10642, Appli
46	7	1.3	127	4	US-09-489-039A-13540	Sequence 13540, Appli
47	7	1.3	136	4	US-09-513-999C-6210	Sequence 6210, Appli
48	7	1.3	157	4	US-09-270-767-44201	Sequence 44201, Appli
49	7	1.3	157	4	US-09-270-767-61037	Sequence 61037, Appli
50	7	1.3	165	1	US-08-413-803-29	Sequence 29, Appli
51	7	1.3	174	5	PCT-US95-03776-27	Sequence 27, Appli
52	7	1.3	187	3	US-08-194-185-1	Sequence 1, Appli
53	7	1.3	195	1	US-08-388-779A-4	Sequence 4, Appli
54	7	1.3	195	1	US-08-591-070A-4	Sequence 4, Appli
55	7	1.3	195	2	US-08-927-855-4	Sequence 44, Appli
56	7	1.3	195	4	US-09-198-552A-444	Sequence 44, Appli
57	7	1.3	199	4	US-09-248-796A-16632	Sequence 16632, Appli
58	7	1.3	200	4	US-09-438-185A-427	Sequence 427, Appli
59	7	1.3	204	4	US-09-549-831-6	Sequence 6, Appli
60	7	1.3	218	4	US-09-270-767-45231	Sequence 45231, Appli
61	7	1.3	225	4	US-09-540-236-798	Sequence 2798, Appli
62	7	1.3	228	4	US-09-252-991A-23718	Sequence 23718, Appli
63	7	1.3	232	4	US-09-270-767-45527	Sequence 45527, Appli
64	7	1.3	234	4	US-09-198-452A-156	Sequence 156, Appli
65	7	1.3	251	4	US-09-540-236-2306	Sequence 2306, Appli
66	7	1.3	251	4	US-09-252-991A-1642	Sequence 1642, Appli
67	7	1.3	252	4	US-09-438-185A-139	Sequence 139, Appli
68	7	1.3	254	4	US-09-438-185A-139	Sequence 13744, Appli
69	7	1.3	260	4	US-09-252-991A-32744	Sequence 11328, Appli
70	7	1.3	265	4	US-09-489-039A-11328	Sequence 7, Appli
71	7	1.3	279	3	US-08-549-515-7	Sequence 1, Appli
72	7	1.3	282	4	US-09-198-552-3800	Sequence 4120, Appli
73	7	1.3	287	4	US-09-107-433-4100	Sequence 28572, Appli
74	7	1.3	291	4	US-09-252-991A-28572	Sequence 15018, Appli
75	7	1.3	301	4	US-09-902-540-15018	Sequence 16767, Appli
76	7	1.3	302	4	US-08-67-607-3	Sequence 3, Appli
77	7	1.3	303	2	US-08-64-362-3	Sequence 3, Appli
78	7	1.3	303	2	US-08-850-392-3	Sequence 3, Appli
79	7	1.3	303	2	US-08-522-714-16	Sequence 16, Appli
80	7	1.3	307	4	US-09-489-039A-10116	Sequence 10116, Appli
81	7	1.3	310	4	US-09-248-796A-17322	Sequence 17322, Appli
82	7	1.3	312	3	US-08-875-533-67	Sequence 67, Appli
83	7	1.3	312	4	US-09-252-991A-22205	Sequence 22205, Appli
84	7	1.3	321	4	US-09-107-433-4282	Sequence 4282, Appli
85	7	1.3	328	3	US-08-875-533-37	Sequence 3, Appli
86	7	1.3	332	3	US-08-875-533-1	Sequence 2, Appli
87	7	1.3	332	3	US-08-875-533-2	Sequence 2, Appli
88	7	1.3	332	3	US-08-875-533-3	Sequence 3, Appli
89	7	1.3	332	3	US-08-875-533-4	Sequence 4, Appli
90	7	1.3	332	3	US-08-975-533-5	Sequence 5, Appli
91	7	1.3	332	3	US-08-875-533-6	Sequence 6, Appli
92	7	1.3	332	3	US-08-875-533-7	Sequence 7, Appli
93	7	1.3	332	3	US-08-875-533-8	Sequence 8, Appli
94	7	1.3	332	3	US-08-875-533-9	Sequence 9, Appli
95	7	1.3	332	3	US-08-875-533-10	Sequence 10, Appli
96	7	1.3	332	3	US-08-975-533-11	Sequence 11, Appli
97	7	1.3	332	3	US-08-875-533-12	Sequence 12, Appli
98	7	1.3	332	3	US-08-875-533-13	Sequence 13, Appli
99	7	1.3	332	3	US-08-875-533-14	Sequence 14, Appli
100	7	1.3	332	4	US-09-462-941-7	Sequence 7, Appli

1.01	7	1.3	4	US-09-510-238A-3	Sequence 3, Appli	Sequence 29359, A
1.02	7	1.3	5	PCT-US95-02776-25	Sequence 25, Appli	Sequence 2, Appli
1.03	7	1.3	5	US-08-482-185A-7	Sequence 7, Appli	Sequence 4, Appli
1.04	7	1.3	4	US-09-134-000C-3742	Sequence 3742, Appli	Sequence 1108, A
1.05	7	1.3	4	US-09-949-016-9639	Sequence 9639, Appli	Sequence 4, Appli
1.06	7	1.3	4	US-09-252-091A-26643	Sequence 26643, A	Sequence 1268, A
1.07	7	1.3	3	US-08-843-330B-11	Sequence 31, Appli	Sequence 2, Appli
1.08	7	1.3	3	US-09-636-728-28	Sequence 28, Appli	Sequence 2, Appli
1.09	7	1.3	3	US-08-330-517-2	Sequence 2, Appli	Sequence 2, Appli
1.10	7	1.3	3	US-08-347-029-4	Sequence 2, Appli	Sequence 2, Appli
1.11	7	1.3	3	US-08-348-779A-2	Sequence 2, Appli	Sequence 2, Appli
1.12	7	1.3	3	US-08-484-246-1	Sequence 1, Appli	Sequence 2, Appli
1.13	7	1.3	3	US-08-591-070A-2	Sequence 2, Appli	Sequence 2, Appli
1.14	7	1.3	3	US-08-113-003-25	Sequence 25, Appli	Sequence 2, Appli
1.15	7	1.3	3	US-08-321-488A-25	Sequence 25, Appli	Sequence 2, Appli
1.16	7	1.3	3	US-08-414-161B-2	Sequence 4, Appli	Sequence 2, Appli
1.17	7	1.3	3	US-08-348-727-2	Sequence 2, Appli	Sequence 2, Appli
1.18	7	1.3	3	US-08-457-254-4	Sequence 6, Appli	Sequence 6, Appli
1.19	7	1.3	3	US-08-927-855-2	Sequence 2, Appli	Sequence 2, Appli
1.20	7	1.3	3	US-08-482-212-2	Sequence 2, Appli	Sequence 2, Appli
1.21	7	1.3	3	US-08-471-045-55	Sequence 25, Appli	Sequence 25, Appli
1.22	7	1.3	3	US-08-469-712A-35	Sequence 2, Appli	Sequence 2, Appli
1.23	7	1.3	3	US-08-999-927-2	Sequence 2, Appli	Sequence 2, Appli
1.24	7	1.3	3	US-08-999-927-6	Sequence 6, Appli	Sequence 6, Appli
1.25	7	1.3	3	US-08-927-819-2	Sequence 2, Appli	Sequence 2, Appli
1.26	7	1.3	3	US-08-461-819-6	Sequence 6, Appli	Sequence 6, Appli
1.27	7	1.3	3	US-08-446-971-55	Sequence 55, Appli	Sequence 55, Appli
1.28	7	1.3	3	US-08-468-910-55	Sequence 55, Appli	Sequence 55, Appli
1.29	7	1.3	3	US-08-761-907-55	Sequence 55, Appli	Sequence 55, Appli
1.30	7	1.3	4	US-09-872-702-13	Sequence 13, Appli	Sequence 13, Appli
1.31	7	1.3	5	PCT-US94-08086-19	Sequence 19, Appli	Sequence 19, Appli
1.32	7	1.3	5	PCT-US94-08086-19	Sequence 29, Appli	Sequence 29, Appli
1.33	7	1.3	5	PCT-US95-01829-29	Sequence 2, Appli	Sequence 2, Appli
1.34	7	1.3	5	PCT-US95-01829-6	Sequence 6, Appli	Sequence 6, Appli
1.35	7	1.3	5	PCT-US95-14932-4	Sequence 5, Appli	Sequence 5, Appli
1.36	7	1.3	5	PCT-US95-16626-4	Sequence 4, Appli	Sequence 4, Appli
1.37	7	1.3	5	PCT-US95-16626-6	Sequence 13, Appli	Sequence 13, Appli
1.38	7	1.3	4	US-09-248-796A-26034	Sequence 6, Appli	Sequence 6, Appli
1.39	7	1.3	4	US-09-252-091A-16624	Sequence 26034, A	Sequence 26034, A
1.40	7	1.3	4	US-09-543-0781A-7864	Sequence 16628, A	Sequence 16628, A
1.41	7	1.3	4	US-08-311-023-2	Sequence 7864, Appli	Sequence 7864, Appli
1.42	7	1.3	4	US-09-252-091A-20861	Sequence 2, Appli	Sequence 2, Appli
1.43	7	1.3	4	US-09-489-039A-10553	Sequence 20861, A	Sequence 20861, A
1.44	7	1.3	4	US-09-411-132A-8	Sequence 10553, A	Sequence 10553, A
1.45	7	1.3	4	US-09-902-040-15789	Sequence 8, Appli	Sequence 8, Appli
1.46	7	1.3	4	US-09-864-085-2	Sequence 15789, A	Sequence 15789, A
1.47	7	1.3	4	US-09-252-091A-22555	Sequence 234, Appli	Sequence 234, Appli
1.48	7	1.3	4	US-09-583-110-3685	Sequence 22555, A	Sequence 22555, A
1.49	7	1.3	4	US-09-270-167-5540	Sequence 3685, Appli	Sequence 3685, Appli
1.50	7	1.3	4	US-09-915-181A-6	Sequence 45540, A	Sequence 45540, A
1.51	7	1.3	4	US-09-248-796A-16849	Sequence 6, Appli	Sequence 6, Appli
1.52	7	1.3	4	US-09-435-034-2	Sequence 16849, A	Sequence 16849, A
1.53	7	1.3	4	US-08-864-085-1	Sequence 2, Appli	Sequence 2, Appli
1.54	7	1.3	4	US-09-613-03-51	Sequence 51, Appli	Sequence 51, Appli
1.55	7	1.3	4	US-10-267-11-51	Sequence 51, Appli	Sequence 51, Appli
1.56	7	1.3	4	US-08-438-064-2	Sequence 7, Appli	Sequence 7, Appli
1.57	7	1.3	4	US-08-441-139-7	Sequence 2, Appli	Sequence 2, Appli
1.58	7	1.3	4	US-08-282-141-2	Sequence 2, Appli	Sequence 2, Appli
1.59	7	1.3	4	US-08-435-034-2	Sequence 2, Appli	Sequence 2, Appli
1.60	7	1.3	4	US-08-436-034-2	Sequence 2, Appli	Sequence 2, Appli
1.61	7	1.3	4	US-08-628-047-2	Sequence 5, Appli	Sequence 5, Appli
1.62	7	1.3	4	US-08-402-053-2	Sequence 27790, A	Sequence 27790, A
1.63	7	1.3	4	US-09-252-091A-27790	Sequence 2, Appli	Sequence 2, Appli
1.64	7	1.3	4	US-09-443-066B-2	Sequence 2, Appli	Sequence 2, Appli
1.65	7	1.3	4	US-09-252-091A-20348	Sequence 20348, A	Sequence 20348, A
1.66	7	1.3	4	US-09-252-091A-21106	Sequence 21106, A	Sequence 21106, A
1.67	7	1.3	4	US-09-252-091A-26839	Sequence 26839, A	Sequence 26839, A
1.68	7	1.3	4	US-09-642-034-5	Sequence 5, Appli	Sequence 5, Appli
1.69	7	1.3	4	US-09-252-091A-16104	Sequence 16014, A	Sequence 16014, A
1.70	7	1.3	4	US-09-248-096A-16104	Sequence 5, Appli	Sequence 5, Appli
1.71	7	1.3	4	US-09-532-091A-32975	Sequence 6142, A	Sequence 6142, A
1.72	7	1.3	4	US-09-248-096A-14723	Sequence 14723, A	Sequence 14723, A
1.73	7	1.3	4	US-09-949-016-8286	Sequence 6964, Ap	Sequence 6964, Ap

GenCore version 5.1.6  
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OM protein - protein search, using SW model

Run on: July 9, 2005, 06:29:52 ; search time 116.974 Seconds

(without alignments)  
 1772.222 Million cell updates/sec

Title: US-09-776-865-2

Perfect score: 536

Sequence: 1 MAAGAMTPDRPVQPARPGGF.....LFAKGEVONWALNDHGHHRH 536

Scoring table: OLIGO

Gapext 6.0.0 , Gapext 60.0

Searched: 2105692 seqs, 386760381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 200000000000

Post-processing: Listing first 1000 summaries

Database : A\_Geneseq\_16Dec04:\*

1: geneseqD1980s:\*

2: geneseqD1990s:\*

3: geneseqD2000s:\*

4: geneseqD2001s:\*

5: geneseqD2002s:\*

6: geneseqD2003as:\*

7: geneseqD2003bs:\*

8: geneseqD2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	536	100.0	536	3	AAY45089	Aay45089 Human GBS
2	536	100.0	536	4	AAB06518	Aae06518 Human gro
3	495	92.4	495	3	AAY45087	Aay45087 Partial h
4	495	92.4	495	4	AAB66967	Aab66967 Human AST
5	495	92.4	495	8	ADJ75516	Adj75516 Marker ge
6	495	92.4	495	8	ADR14587	Adr14587 Human NP-
7	495	92.4	495	8	ADP25217	Adp25217 PRO polyp
8	394	73.5	495	4	AAM38959	Aam38959 Human pol
9	314	58.6	314	4	AAG65238	Aag65238 Human pol
10	304	56.7	309	4	AAM40745	Aam40745 Human pol
11	284	53.0	284	5	ABP1345	Abp1345 Human ova
12	273	50.9	277	4	AAM93914	Aam93914 Human pol
13	273	50.9	277	8	ADJ32036	Adj32036 Human pro
14	217	40.5	272	5	ABP89975	Abp89975 Human pol
15	180	33.6	194	4	AAM25685	Aam25685 Human pro
16	144	26.9	343	4	ABG12999	Abg12999 Novel hum
17	144	26.9	343	6	ABG00820	Abg00820 Polypepti
18	134	25.0	256	4	ABG02032	Abg02032 Novel hum
19	124	23.1	124	4	AAGB1307	Aagb1307 Human AFP
20	61	11.4	495	3	AAY45088	Aay45088 Sheep GBS
21	61	11.4	495	4	AAE06519	Aae06519 Sheep gro
22	15	2.8	15	4	AAG65239	Aag65239 Human sod
23	14	2.6	495	3	AAY45090	Aay45090 Human She
24	11	2.1	467	8	ADD12952	Adp12952 Protein e
			578	7	ADG88331	Adg88331 Rat trans

2.1	582	4	AM79273	Human Pro
2.1	582	6	ABG74796	Rat DNP1
2.1	582	6	ABG74795	Human DNP
2.1	582	6	ABG74797	Murine DN
2.1	582	6	ABM04787	Rat Na-de
3.1	582	7	ADC15494	Mouse DNP
3.2	582	7	ADC15492	Rat DNPI
3.3	582	7	ADC15490	Human DNP
3.4	582	7	ADD01475	Human VGL
3.5	582	8	ADP29764	Rat sec
3.6	582	8	AAW78919	Human hae
3.7	582	7	ADF90914	Human hep
3.8	544	8	ADN32240	Bacterial
3.9	573	8	ADN23219	Bacterial
4.0	573	8	ADN23218	Bacterial
4.1	49	1.7	ABT70143	Drosophil
4.2	8	1.5	ABG28472	Novel hum
4.3	8	1.5	ABU28455	Protein e
4.4	8	1.5	ADM04596	Human pro
4.5	8	1.5	ADBB80215	Mycobacte
4.6	8	1.5	AAG39966	Arabidops
4.7	8	1.5	ARG14816	Arabidops
4.8	8	1.5	AAG39935	Arabidops
4.9	8	1.5	AAG14815	Arabidops
5.0	8	1.5	ADG95882	B. faeciu
5.1	8	1.5	ADG44934	Bacterial
5.2	8	1.5	ABB70142	Drosophil
5.3	8	1.5	ABO72850	Pseudomon
5.4	8	1.5	ABB65873	Drosophil
5.5	8	1.5	ABB60525	Drosophil
5.6	8	1.5	ABG3994	3
5.7	8	1.5	AAG14814	Arabidops
5.8	8	1.5	ABB58701	Drosophil
5.9	8	1.5	AW05148	Human bra
6.0	8	1.5	AWT05010	Human sod
6.1	8	1.5	ABG74794	Murine BN
6.2	8	1.5	ABG74793	Rat BNPI
6.3	8	1.5	ABG74732	Human BNP
6.4	8	1.5	ABG74791	Human BNP
6.5	8	1.5	ADG15488	Mouse BNP
6.6	8	1.5	ADC15484	Human BNP
6.7	8	1.5	ADC15482	Human BNP
6.8	8	1.5	ADC15486	Rat BNPI
6.9	8	1.5	ADD01474	Human VGL
7.0	8	1.5	ADJ95072	Novel NOV
7.1	8	1.5	AO13870	Human pol
7.2	8	1.5	AAU99329	Human tra
7.3	8	1.5	AAO3094	Human tra
7.4	8	1.5	ADG88329	Human tra
7.6	8	1.5	ADG88339	Human tra
7.7	8	1.5	ADR10021	Human pro
7.8	7	1.5	ABO77441	Pseudomon
7.9	8	1.5	ABB07689	Rat gluta
8.0	8	1.5	ABD63934	Drosophil
8.1	8	1.5	ABB65890	Drosophil
8.2	8	1.5	ADBB85120	Mouse DNA
8.3	8	1.5	ABP81116	Rat TPO
8.4	8	1.5	ABP81117	Human TPO
8.5	7	1.3	ABP81115	Human TPO
8.6	7	1.3	AY88326	Human Cat
8.7	7	1.3	ADC39960	Yellow gr
8.8	7	1.3	AY88323	Human Cat
8.9	7	1.3	AY03007	Fragment
9.0	7	1.3	ADA07542	Human sec
9.1	7	1.3	ADN41322	Novel hum
9.2	7	1.3	ADG64744	Gene i
9.3	7	1.3	AAY88336	Human Cat
9.4	7	1.3	AAU89268	Insulin/i
9.5	7	1.3	ABJ25329	SAC isola
9.6	7	1.3	ABP81111	Rat sec
9.7	7	1.3	Aau90770	Insulin/i
9.8	7	1.3	AAR81401	Artificia
9.9	7	1.3	ABG24500	Rat trans
10.0	7	1.3	ADG38279	Gene 20 h

99	7	1.3	AAB40211	Gene 17 h	172	7	1.3	ADM09216	Human TPO
100	7	1.3	AAB65452	Propionib	173	7	1.3	AAR81348	[His33, T
101	7	1.3	ABM61971	Propionib	174	7	1.3	AAR81349	[His33, A
102	7	1.3	AAB40931	Propionib	175	7	1.3	AAR81352	[Gly16, E
103	7	1.3	ABM37450	Propionib	176	7	1.3	AAR81350	[His33, G
104	7	1.3	AAM95790	Human rep	177	7	1.3	AAR81351	[Gly16, E
105	7	1.3	ABB96321	Human tes	178	7	1.3	AAR81351	[Gly16, E
106	7	1.3	ABP08020	Human ORF	179	7	1.3	AAW04868	Human thr
107	7	1.3	AAM16057	Peptide #	180	7	1.3	AAR99468	Human Thr
108	7	1.3	ABB35049	Peptide #	181	7	1.3	AAY5013	Human wil
109	7	1.3	ABM28854	Peptide #	182	7	1.3	ABP78104	N. gonorr
110	7	1.3	ABP29854	Peptide #	183	7	1.3	ADC54795	Human thr
111	7	1.3	ABB20461	Protein #	184	7	1.3	AAR97764	Human thr
112	7	1.3	ABM68235	Human bon	185	7	1.3	AAR97770	Human thr
113	7	1.3	AAM5884	Human bra	186	7	1.3	AAR97765	Human thr
114	7	1.3	ABG49886	Human liv	187	7	1.3	AAR80823	Human MGD
115	7	1.3	ABM03784	Peptide #	188	7	1.3	Aay12953	[IN30, T32,
116	7	1.3	ABG37771	Human pep	189	7	1.3	ABP78104	N. gonorr
117	7	1.3	AAB65993	Human sec	190	7	1.3	AAR97771	Human thr
118	7	1.3	ABG2278	Arbidiops	191	7	1.3	AAB81390	Human thr
119	7	1.3	AGG2784	Novel hum	192	7	1.3	Abr97770	Human thr
120	7	1.3	AAG82749	S. epider	193	7	1.3	AAR97766	Human thr
121	7	1.3	ABM84646	Human imm	194	7	1.3	AAP0694	Sequence
122	7	1.3	ABM4545	Human pro	195	7	1.3	AAR97772	Human thr
123	7	1.3	ADH32514	Yeast smO	196	7	1.3	ADC39950	Yellow gr
124	7	1.3	ADK35339	Novel hum	197	7	1.3	AAP0616	Fish grow
125	7	1.3	ADQ65018	Novel hum	198	7	1.3	ABP81244	Sequence
126	7	1.3	AAM49390	Actinomad	199	7	1.3	Aaw1372	Synthetic
127	7	1.3	ABP31660	Human ORF	200	7	1.3	AAP90594	Aam4919
128	7	1.3	AAG22277	Arbidiops	201	7	1.3	AAR0735	Korean ro
129	7	1.3	AAG08053	Arabidops	202	7	1.3	AAR24137	Fish grow
130	7	1.3	ADK31539	Partial p	203	7	1.3	ABM80182	Tumour-as
131	7	1.3	ABP0142	Staphyloc	204	7	1.3	Aar99859	Truncated
132	7	1.3	ADP07186	Staphyloc	205	7	1.3	Aay06827	Human tru
133	7	1.3	ABP21660	Human ORF	206	7	1.3	AAY5026	Chlamydia
134	7	1.3	AAG22277	Arbidiops	207	7	1.3	ABP0732	Fish grow
135	7	1.3	AAU20576	Human sec	208	7	1.3	Aaw12954	[IN30, T32,
136	7	1.3	ADP07186	Partial p	209	7	1.3	Abr97782	Spotted f
137	7	1.3	ADN25718	Hyperther	210	7	1.3	AAB59504	Human sec
138	7	1.3	ABG11406	Novel hum	211	7	1.3	ADC84463	Drosophili
139	7	1.3	ABM9101	Human rep	212	7	1.3	AAP0617	Fish grow
140	7	1.3	AAG02129	Human sec	213	7	1.3	AAP90732	Fish grow
141	7	1.3	Aaw94926	Human phe	214	7	1.3	Aau7728	Korean ro
142	7	1.3	ABR80822	Human MGD	215	7	1.3	AAB59538	Spotted f
143	7	1.3	ADP07186	Hyperther	216	7	1.3	AAB95638	Human sec
144	7	1.3	ABG11406	Novel hum	217	7	1.3	AAB95638	Spotted f
145	7	1.3	ABP21660	Human ORF	218	7	1.3	AAB95638	Human sec
146	7	1.3	AAG74756	Human col	219	7	1.3	AAB95638	Spotted f
147	7	1.3	ADR10198	Human pro	220	7	1.3	AAB95638	Human sec
148	7	1.3	ABR80822	Human thr	221	7	1.3	AAB95638	Spotted f
149	7	1.3	ADP07186	Human pro	222	7	1.3	AAB95638	Human sec
150	7	1.3	ABG11406	Delta Ar	223	7	1.3	AAB95638	Spotted f
151	7	1.3	ABP24501	Human sec	224	7	1.3	AAB95638	Human sec
152	7	1.3	AAG74756	Human col	225	7	1.3	AAB95638	Spotted f
153	7	1.3	ADR10198	Human pro	226	7	1.3	AAB95638	Human sec
154	7	1.3	ABR80822	Human thr	227	7	1.3	AAB95638	Spotted f
155	7	1.3	ADP07186	Protein e	228	7	1.3	AAB95638	Spotted f
156	7	1.3	ABG11406	Delta Ar	229	7	1.3	AAB9773	Human thr
157	7	1.3	ABP24501	Human sec	230	7	1.3	AAB88434	Breast an
158	7	1.3	AAG74756	Human col	231	7	1.3	ADC31328	Human nov
159	7	1.3	ADR10198	Human pro	232	7	1.3	ADR09364	Human pro
160	7	1.3	ABR80822	Human thr	233	7	1.3	Abh88411	Enterococ
161	7	1.3	ADP07186	Human pro	234	7	1.3	Abm68944	Photobab
162	7	1.3	ABG11406	[Arg131]T	235	7	1.3	AAB56768	Human pro
163	7	1.3	ABP24501	[Ala1, Va	236	7	1.3	Aao15070	Humicola
164	7	1.3	AAG74756	[Ala1, Va	237	7	1.3	AAG80602	Humicola
165	7	1.3	ADR10198	[Ala1, Va	238	7	1.3	ADC32999	Human nov
166	7	1.3	ABR80822	[Leu146]T	239	7	1.3	Ago09434	Arabidops
167	7	1.3	ADP07186	[Ala1, Va	240	7	1.3	Ago08052	Arabidops
168	7	1.3	ABG11406	[Ala1, Va	241	7	1.3	ABG16682	Novel hum
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US-09-776-865-4 (1-495) x CR618872 (1-3189)

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Db 136 CCTCTCTACGGCCGCCCAAGGGCGAACCGCTCCACAGTCGTGCTGCTGTTAC 195
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Db 436 ATCACACAGATTCCTGGAGATATGGCTGAGAAATGGCTAGTAGA 495
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Db 976 TACACTGACATTTATCTTATCTTATGACATTATGAGAGGATCCPA 1035
Qy 321 ArgPheAsnIleGlnGluAsnGlyPheLeuSerAlaValProTyrlleGlyCysTrpLeu 340
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full insert sequence.
AK029102 VERSION GI:26325087
HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
Carninci, P. and Hayashizaki, Y.
AUTHORS
TITLE Meth. Enzymol. 303, 19-44 (1999)
JOURNAL
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kojima, H., Okazaki, Y., Muranatsu, M. and Hayashizaki, Y.
AUTHORS
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
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Shibata, K., Itoh, M., Aizawa, K., Nagaoaka, S., Sasaki, N., Carninci, P., Authors

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GenCore version 5.1.6  
(c) 1993 - 2005 Compugen Ltd.

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Listing first 45 summaries

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9	2329	89.0	3362	10 US-09-814-353-19097	Sequence 19057, A
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#### ALIGNMENTS

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RESULT 1
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Sequence 3, Application US/09776865
; Patent No. US20020061846A1
; GENERAL INFORMATION:
; APPLICANT: Hellbergist, Carl
; TITLE OF INVENTION: Methods for Preventing or Attenuating Pathoangiogenic Conditions
; FILE REFERENCE: 22100-0100
; CURRENT APPLICATION NUMBER: US/09/776,865
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 2000-02-02
; PRIOR FILING DATE: 2000-02-02
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 2844
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; ORGANISM: Ovis sp.  
; FEATURE: CDS  
; NAME/KEY: CDS  
; LOCATION: (84) .. (1568)  
; US-09-776-865-3

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Score: 2617.00 Matches: 495  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
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; GENERAL INFORMATION:  
; APPLICANT: Hellergquist, Carl  
; ADDRESS: Fu, Changlin  
; TITLE OF INVENTION: GBS Toxin Receptor  
; FILE REFERENCE: CAB-B-008/01/US  
; CURRENT APPLICATION NUMBER: US/10/823-506  
; CURRENT FILING DATE: 2004-04-12  
; PRIOR APPLICATION NUMBER: US/09/359,167  
; PRIOR FILING DATE: 1999-07-21  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60-693,843  
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GenCore version 5.1.6  
 Copyright (c) 1993 - 2005 Compugen Ltd.

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Title: US-09-776-865-4

Perfect score: 2617

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 -NO\_MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DEBLOCK=100 -LONGLOG  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2617	100.0	2844	4 US-09-359-167-3	Sequence 3, Appli
2	2329	89.0	2513	4 US-09-949-016-1834	Sequence 1, Appli
3	2329	89.0	2602	4 US-09-359-167-1	Sequence 1831, Appli
4	2329	89.0	2930	4 US-09-359-167-7	Sequence 1, Appli
5	1971	84.9	1485	4 US-09-359-167-9	Sequence 7, Appli
6	980	37.4	1811	4 US-09-740-167-11	Sequence 9, Appli
7	956.5	36.5	2607	4 US-09-915-181A-1	Sequence 11, Appli
8	932	35.6	2366	4 US-09-949-016-5483	Sequence 1, Appli
9	931	35.6	2716	1 US-08-647-484-1	Sequence 1, Appli
10	931	35.6	2716	1 US-08-647-484-3	Sequence 3, Appli
11	931	35.6	2716	1 US-08-647-481-1	Sequence 1, Appli
12	931	35.6	2716	1 US-08-647-481-7	Sequence 1, Appli

## ALIGNMENTS

RESULT 1  
 US-09-359-167-3  
 ; Sequence 3, Application US/09359167  
 ; Patent No. 6803448  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hellqvist, Carl  
 ; TITLE OF INVENTION: GBS Toxin Receptor  
 ; FILE REFERENCE: CARB 008/01US  
 ; CURRENT APPLICATION NUMBER: US/09/359,167  
 ; CURRENT FILING DATE: 1999-07-21  
 ; EARLIER APPLICATION NUMBER: 60-693,843  
 ; EARLIER FILING DATE: 1998-07-22  
 ; NUMBER OF SEQ ID NOS: 12  
 ; SOFTWARE: PatentIn Ver. 2.0  
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 ; LENGTH: 2844  
 ; TYPE: DNA  
 ; ORGANISM: Ovis sp.  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (84)..(1568)  
 ; US-09-359-167-3

Alignment Scores:  
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 Conservative: 0  
 Mismatches: 0  
 Indels: 0  
 Gaps: 0  
 US-09-776-865-4 (1-495) x US-09-359-167-3 (1-2844)  
 Qy 1 MetlySerProValSerAspIeuAlaProSerAspGlySerAspArgThr 20



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: July 9, 2005, 02:43:23 ; Search time 742.26 Seconds

(without alignments)

3947.771 Million cell updates/sec

Title: US-09-776-865-4

Perfect score: 2617

Sequence: 1 MKSPVSDLAPSDEGGESDRT.....LFAKGEVQNVNAISDHQHGRN 495

Scoring table: BLOSUM62

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Ygapop 10.0 Ygapbext 0.5  
Fgapop 6.0 Fgapbext 7.0  
Delop 6.0 Delbext 7.0

Searched:

4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters:

8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-LOCPDX=0 -UNITS=bits -START=1 -END=1 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR SCORE=0.25 -THR MAX=100 -THR MIN=0 -ALIGN=15
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-USER=US09776865@CEN.1 -1.1014@runat 08072005 175548 23365 -NCFU=6 -ICPU=3
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-DEV TIMEOUT=30 -WARN -TIMEOUT=30 -THREADES=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -XGAPOP=10 -XGAPEXT=0.5 -DELEXT=7
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Database : N\_Geneset\_16Dec04:\*

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RESULT 1

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XX AC AA250876;
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31-MAY-2000 (first entry)

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XX DE Sheep GBS toxin receptor (SP55) cDNA.
XX AC AA250876;
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XX KW Sheep GBS toxin receptor; group B beta-haemolytic streptococci; SP55;
KW pathophysiological vascularisation; cancer metastases; angiogenesis;
KW neovascularisation; reperfusion injury; scarring; keloid;
KW chronic inflammation; rheumatoid arthritis; psoriasis; neural injury;
KW endothelial cell proliferation; antibacterial; anticancer;
KW anti-angiogenic; anti-inflammatory; anti-arthritis; anti-psoriatic; ss.
OS XX Ovis sp.
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SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Location/Qualifiers
1	2617	100.0	2844	3 AAZ50876	Aaz50876 Sheep GBS	XX PN
2	2617	100.0	2844	4 ADD10326	ADD10326 Sheep gro	XX PD
3	2329	89.0	2511	12 ADQ81158	ADD14158 Human tum	XX PD
4	2329	89.0	2512	4 AAF5590	Aaf5590 Human AST	XX PF
5	2329	89.0	2602	3 AAZ50875	AAZ50875 Partial h	XX PF

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## ALIGNMENTS

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Add01462 Mouse TCH
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Add014
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X	22-JUL-1998;	98US-0093843P.		
X	(UVA-)	UNIV VANDERBILT.		
X	Hellerqvist CG,	Fu C;		
X	WPI: 2000-205377/18.	P-PSDB; AY45088.		
X	New polynucleotide encoding mammalian receptor for streptococcus toxin, useful for diagnosis and treatment of, e.g. pneumonia in neonates.			
X	Claim 3; Page 83-86; 109pp; English.			
X	The present cDNA sequence encodes partial sheep GBS (group B beta - haemolytic streptococci) toxin receptor (SP5E). This sequence was cloned using a primary culture of sheep lung endothelial cells. Expression vectors comprising this cDNA can be transformed into host cells to express GBS toxin receptor and its fragments. Detecting the receptor in tissues is used to diagnose pathological vascularisation, e.g. for detecting cancer metastases. GBS toxin receptors are useful for treating conditions associated with pathological angiogenesis or neovascularisation (specifically cancer, reperfusion injury, scarring during wound healing, keloids, chronic inflammation (rheumatoid arthritis or psoriasis) or neural injury), and to raise specific antibodies used for treating early onset disease. Inhibitors of this receptor are useful for treating pathological or hypoxia-induced endothelial cell proliferation and migration.			
X	Sequence 2844 BP; 745 A; 623 C; 594 G; 882 T; 0 U; 0 Other;			
X	Alignment Scores:			
X	Score: 5.998-256	Length: 2844		
X	Score: 2617.00	Matches: 495		
X	Percent Similarity: 100.00%	Conservative: 0		
X	Percent Local Similarity: 100.00%	Mismatches: 0		
X	Query Match: 100.00%	Indels: 0		
X	DB: 3	Gaps: 0		
X	S-09-776-865-4 (1-495) x AAZ50876 (1-2844)			
X	1 MetLysSerProValSerAspLeuAlaProSerAspGlyGluGlySerAspArgThr 20	Qy	Length: 2844	
X	84 ATGAGTCCGGTTCGGACTTAACCCAGCGAGGGCTGGACCGCACA 143	Db	Score: 2617.00	
b	21 ProLeuLeuGlnArgAlaProArgAlaGluProAlaProValCysSerAlaargTyr 40	Qy	Matches: 495	
b	144 CCGCTCTGGCGCCGGAAACCCGGTCCACTATGCTGCTGCTGTTAC 203	Db	Mismatches: 0	
b	41 AsnLeuAlaPheLeuSerphepheGlyphepheValLeuThrSerLeuArgValLeu 60	Qy	Indels: 0	
b	204 AACCTAGCATTTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCT 263	Db	Gaps: 0	
b	61 SerValAlaLeuValAspMetValAspSerAsnThrAlaLysAspAsnArgThrSer 80	Qy		
b	264 AGCTTGCACTAGTGCACTGGATCAACAAACAGATATAAGCTGCC 323	Db		
b	81 TyrGluCysAlaGluHisSerAlaProIleLeuLeuLysAsnGlnThrGlyLysLys 100	Qy		
b	324 TACGGTGTCAAGCATTGTCTGCCATAAAAGTCTCACAACCAAACGGTAAAGA 383	Db		
b	101 TyrArgTrpAspAlaGluThrGlnGlyLysTyrLeuGlySerphepheValGlyTyrIle 120	Qy		
b	384 TACCGTGTGGATGCGAAACTCAAGATGGATTCTGGATCTTCTTGTACATC 443	Db		
b	121 IleThrGlnIleProGlyGlyTyrValAlaSerArgSerGlyLysIleLeuIeGly 140	Qy		
b	444 ATCACACAAATTCTGGCCATAGTGATCAATGTTGGTCACTTTC 503	Db		
b	141 PheGlyIlePheAlaThrAlaIlePheLeuThrProLeuAlaAspPheGly 160			RESULT 2
b	504 TTCCGGATCTTGTCAAGGTTCTCACCCCTGTCACCCCTGTCAGAATTTCGG 563			AAD10326
b				standard; DNA: 2844 bp.
b				ID AAD10326
b				XX





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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: July 9, 2005, 03:19:49 ; Search time 4969.57 Seconds

(without alignments)

4105.478 Million cell updates/sec

US-09-776-865-2

Perfect score: 2836

Sequence: 1 MARGAWTDPRVQDARPGGF.....LPAKGEVONWALNDHGHRRH 536

Scoring table: BIOSTM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Pgapop 6.0 , Pgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 3423954 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing First 45 summaries

Command line parameters:

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-UNITS=bits -START=1 -END=1  
-DOCALIGN=-100 -THR SCORE=0.02 -TRANS=bloom52 -TRANS=human40 -cdd -LIST=45  
-OUTFMT=6 -NORM=ext -HEAPSIZES=500 -MINLEN=0 -MAXLEN=1000 -THR MIN=0  
-USER=US-09-776-865@CCN\_1-1.641.0@runat 08072005.175549 23379 -NCPU=6 -ICPU=3  
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Database : EST:\*

1: 9b\_est1:\*

2: 9b\_est2:\*

3: 9b\_htc:\*

4: 9b\_est3:\*

5: 9b\_est4:\*

6: 9b\_est5:\*

7: 9b\_est6:\*

8: 9b\_gbs1:\*

9: 9b\_gbs2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result No.	Query	Match	Length	DB	ID	Description
1	2752	97.0	3189	3	CR18872	CR18872 full-length
2	2312	81.5	3202	3	AK029102	AK029102 Mus muscu
3	1772	62.5	1051	1	AL550137	AL550137
4	1659.5	59.9	1059	5	BX425026	BX425026
5	1651	58.2	1038	7	BX439809	BX439809
6	134	47.5	947	7	C0579484	C0579484 ILLUMIGEN
7	1236	43.6	754	4	B1907284	B1907284 603063858
8	1183	41.7	737	7	CK833373	CK833373 4057771 B
9	1174.5	41.4	901	6	CD106410	CD106410 AGENCOURT

FEATURES	Source
1. 3189	/organism="Homo sapiens"
2. (bases 1 to 3189)	Genoscope.
3. Direct Submission	Genoscope.
4. COMMENT	Submitted (20-JUN-2004) Genoscope - Centre National de Sequenage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seques@genoscope.cnrs.fr)
5. JOURNAL	Web : <a href="http://www.genoscope.cnrs.fr">www.genoscope.cnrs.fr</a>
6. ACCESSION	1st strand cDNA was primed with a 5'Nt1-oligo(dt) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
7. VERSION	1. (bases 1 to 3189)
8. KEYWORDS	HTC; CNS17 cDNA.
9. SOURCE	Homo sapiens (human)
10. ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
11. REFERENCE	Li W.B., Gruber C., Jessee J. and Polayes D.
12. AUTHORS	Unpublished
13. TITLE	Contact : Peng Liang Email : <a href="mailto:fliang@lifetech.com">fliang@lifetech.com</a> URL : <a href="http://fulllength.invitrogen.com/">http://fulllength.invitrogen.com/</a> Invitrogen Corporation 1600 Faraday Avenue
14. JOURNAL	http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue
15. REMARK	2 (bases 1 to 3189)
16. REFERENCE	2 (bases 1 to 3189)
17. AUTHORS	Genoscope.
18. TITLE	Direct Submission
19. JOURNAL	Submitted (20-JUN-2004) Genoscope - Centre National de Sequenage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seques@genoscope.cnrs.fr)
20. COMMENT	1st strand cDNA was primed with a 5'Nt1-oligo(dt) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
21. JOURNAL	Location/Qualifiers
22. REMARK	1. 3189



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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: July 9, 2005, 07:16:14 ; Search time 910.316 Seconds

(without alignments)

3896.712 Million cell updates/sec

Title: US-09-776-865-2

Perfect score: 2836

Sequence: 1 MAAGMTTPRPPQPARPGGF.....LFAKGEVQNWLNDHGRHRH 536

Scoring table: BIOSUM62

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Ygapop 10.0 Ygapext 0.5

Fgap 6.0 Fgapext 7.0

Delop 6.0 Delext 7.0

Searched: 6330943 seqs, 3139157217 residues

Total number of hits satisfying chosen parameters: 12661886

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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 -DB=Published\_Application\_NA -QFN=fasfrt -SUFFTX=rnpb -MINMATCH=0.1  
 -LOCPL=0 -LOCPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum16  
 -TRANS=human40\_cdi -LIST=45 -DOCALIGN=200 -THR SCORE=opt -THR MAX=100  
 -THR MIN=0 -ALIGN=0 -MODE=LOCAL -OUTENT=ptc -HEAPSIZE=500 -MINLEN=0  
 -MAXLEN=2000000000 -USERID=08072005\_175551\_23472  
 -NCPU=6 -ICPU=3 -NMAP -LARGEQUERY -NNG SCORES=0 -WAIT -DSPBLOCK=100  
 -LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPEXT=0.5  
 -FGAPOP=6 -FGCPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:\*

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2: /cgn2\_6/ptodata/2/pubnra/PCT\_NEW\_PUB.seq:\*

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4: /cgn2\_6/ptodata/2/pubnra/us05\_PUBCOMB.seq:\*

5: /cgn2\_6/ptodata/2/pubnra/us07\_NEW\_PUB.seq:\*

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7: /cgn2\_6/ptodata/2/pubnra/us08\_NEW\_PUB.seq:\*

8: /cgn2\_6/ptodata/2/pubnra/us09\_PUBCOMB.seq:\*

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	2836	100.0	2930	9	US-09-776-865-1		Sequence 1, Appli
2	2836	100.0	2930	21	US-10-823-306-7		Sequence 2, Appli
3	2804	98.9	2626	14	US-10-198-846-12482		Sequence 12482, A
4	2804	98.9	3362	10	US-09-814-353-19097		Sequence 19097, A
5	2770.5	97.7	3329	19	US-10-755-587		Sequence 587, APP
6	2761	97.4	3292	21	US-10-887-553A-858		Sequence 858, APP
7	2717	95.8	2602	21	US-10-823-506-1		Sequence 1, Appli
8	2614	92.2	1488	13	US-10-098-841-22		Sequence 322, APP
9	2338	82.4	2844	21	US-09-776-065-3		Sequence 3, Appli
10	2338	82.4	2844	21	US-10-823-506-3		Sequence 3, Appli
11	2217	78.2	1485	21	US-10-823-506-9		Sequence 11, Appli
12	1967	69.4	1485	21	US-10-823-506-11		Sequence 11, Appli
13	1521	53.6	1872	17	US-10-264-049-302		Sequence 302, APP
14	1515	53.4	1651	17	US-10-264-037-94-6		Sequence 94, APP
15	973	34.3	3982	18	US-10-205-331-8		Sequence 8, Appli
16	973	34.3	3982	20	US-10-734-731-11		Sequence 11, Appli
17	973	34.3	3982	20	US-10-807-500-11		Sequence 11, Appli
18	971	34.2	2528	20	US-10-734-731-13		Sequence 13, Appli
19	971	34.2	2528	20	US-10-807-500-13		Sequence 13, Appli
20	968	34.1	3946	20	US-10-807-500-9		Sequence 9, Appli
21	968	34.1	3946	21	US-10-887-553A-1016		Sequence 1016, Ap
22	968	34.1	3946	21	US-10-233-045-1		Sequence 21, Appli
23	962	33.9	3423	16	US-09-740-041-1		Sequence 1, Appli
24	956	33.7	1811	16	US-10-389-967-1		Sequence 1, Appli
25	956	33.7	1767	22	US-10-499-731-39		Sequence 29, APP
26	955	33.7	1850	22	US-10-499-731-45		Sequence 45, Appli
27	955	33.7	3838	21	US-10-887-553A-1200		Sequence 1200, Ap
28	955	33.7	1803	22	US-10-499-731-57		Sequence 47, APP
29	945	33.3	1822	22	US-10-499-731-58		Sequence 58, APP
30	945	33.3	2716	17	US-10-314-790-6		GENERAL INFORMATION
31	943	33.3	2366	20	US-10-734-731-1		Sequence 1, Appli
32	942.5	33.2	2366	20	US-10-807-500-1		Sequence 1, Appli
33	942.5	33.2	2366	20	US-10-734-731-3		Sequence 3, Appli
34	942	33.2	2716	20	US-10-807-500-3		Sequence 3, Appli
35	942	33.2	2716	18	US-10-287-226-299		Sequence 1, Appli
36	940.5	33.2	1701	18	US-10-296-115-461		Sequence 299, APP
37	940.5	33.2	1975	18	US-10-152-319A-2039		Sequence 2039, APP
38	939	33.1	2024	20	US-10-734-731-5		Sequence 5, Appli
39	939	33.1	2024	20	US-10-807-500-5		Sequence 5, Appli
40	939	33.1	2024	20	US-10-734-731-7		Sequence 7, Appli
41	936	33.0	2836	20	US-10-807-500-7		Sequence 7, Appli
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44	852	30.0	494	10	US-09-814-353-46		Sequence 1289, A
45	837	29.5	498	10	US-09-814-353-46		Sequence 46, APP

#### ALIGNMENTS

RESULT 1	US-09-776-865-1	Sequence 1, Application US/09776865
		; GENERAL INFORMATION:
		; APPLICANT: Hellbergist, Carl
		; TITLE OF INVENTION: Methods for Preventing or Attenuating Pathoangiogenic Conditions
		; FILE REFERENCE: 22100-0100 46126-252687
		; CURRENT APPLICATION NUMBER: US/09-0776,865
		; CURRENT FILING DATE: 2001-02-02
		; PRIOR APPLICATION NUMBER: US 60/179,870
		; PRIOR FILING DATE: 2000-02-02
		; SOFTWARE: PatentIn version 3.0
		; SEQ ID NO 1
		; LENGTH: 2930



GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: July 9, 2005, 06:18:14 : Search time 253.183 Seconds  
 (without alignments)  
 3464.068 Million cell updates/sec

Title: US-09-776-865-2

Perfect score: 2836

Sequence: 1 MAAGAMTPPRVQPARGGF.....LFAKGEVQNNVALNDIHGHRH 536

Scoring table: BL0SUM62

xgapop 10.0 ; Xgapext 0.5  
 Ygapop 10.0 ; Ygapext 0.5  
 Pgapop 6.0 ; Pgapext 7.0  
 Delop 6.0 ; Delext 7.0

Searched: 1202784 seqs, 81838359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing First 45 summaries

Command line parameters: -MODBLI=frame\_plus\_p2n.model  
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 -LOOPEXT=5  
 -UNITS=5  
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 -FGFPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELETE=7

Sequence 1, Appli

Sequence 3, Appli

Sequence 1, Appli

Sequence 1, Appli

Sequence 745, App

Sequence 1390, A

Sequence 660, App

Sequence 18, Appli

Sequence 557, Ap

Sequence 2, Appli

Sequence 19, Appli

Sequence 1182, Ap

Sequence 815, App

Sequence 2492, Ap

Sequence 1395, A

Sequence 1018, Ap

Sequence 13516, A

Sequence 13814, A

Sequence 602, App

Sequence 6462, Ap

Sequence 19, Appli

Sequence 2786, Ap

Sequence 5, Appli

Sequence 11, Appli

Sequence 3032, A

Sequence 2771, Ap

Sequence 3459, Ap

Sequence 1297, Ap

Sequence 16579, A

Sequence 65, Appli

Sequence 2164, Ap

## ALIGNMENTS

RESULT 1  
 US-09-359-167-7

; Sequence 7, Application US/09359167

; Patent No. 6803448

; GENERAL INFORMATION:

; APPLICANT: Hellqvist, Carl

; TITLE OF INVENTION: GBS Toxin Receptor

; FILE REFERENCE: CARB-008/01US

; CURRENT APPLICATION NUMBER: US/09/359,167

; CURRENT FILING DATE: 1999-07-21

; EARLIER APPLICATION NUMBER: 60-693,843

; EARLIER FILING DATE: 1998-07-22

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO: 7

; LENGTH: 2930

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (263) .. (1870)

; US-09-359-167-7

## SUMMARIES

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB ID	Description
1	2836	100.0	2930	4	US-09-359-167-7
2	2804.5	98.9	2513	4	US-09-949-016-1834
3	2717	95.8	2602	4	US-09-359-167-1
4	2338	82.4	2844	4	US-09-359-167-3
5	1967	78.2	1485	4	US-09-359-167-9
6	956	69.4	1485	4	US-09-359-167-11
7	956	33.7	1811	4	US-09-740-041-1
8	942.5	33.2	2366	4	US-09-949-016-5483
9	942	33.2	2716	1	US-08-647-84-1
10	942	33.2	2716	1	US-08-647-84-3
11	942	33.2	2716	1	US-08-647-81-1
12	942	33.2	2716	1	US-08-647-81-3

Length: 2930  
 Matches: 536  
 Conservative: 0  
 Mismatches: 0  
 Indexes: 0  
 Gaps: 0

US-09-776-865-2 (1-536) x US-09-359-167-7 (1-2930)

QY 1 MetAlaAlaGlyAlaMetThrProProArgProValGlyProGlyGlyPhe 20



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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: July 9, 2005, 02:43:23 ; Search time 803.74 Seconds

(without alignments)

3947.771 Million cell updates/sec

Title: US-09-776-865-2

Perfect score: 2836

Sequence: 1 MAGAGMTTPRPPQPARPGGF.....LPAKGEVQNWAINDHICHRH 536

Scoring table: BLOSUM62

Xgapop 10.0 Xgapext 0.5

Ygapop 10.0 Ygapext 0.5

Pgapop 6.0 Pgapext 7.0

Dgapop 6.0 Dgapext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=cgn2.1/USPRO.spool/DS09776865/runat 08072005\_175548\_23365/app\_query.fasta\_1.1358

-DB=N Geneseq\_16Dec04 -QMT=FASTA -SUFFIX=rrg -MINMATCH=0 1 -1COPICL=0

-LOCDEXT=0 UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi

-LIST=45 -DOALIGN=100 -THR SCORE=0.05 -THR MAX=100 -THR MIN=0 -ALIGN=15

-MODE=LOCAL -OUTFORMAT=PTO -HEAPSIZE=500 -MINIFRN=0 -MAXIFRN=2000000000

-USER=US09776865@CGN1\_1\_1004@runat 08072005\_175548\_23365 -NCFLU=6 -ICPU=3

-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -SPBLOCK=100 -LONGLOG

-DEV TIMEOUT=30 -WARN TIMEOUT=30 -THREADES=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6

-FGAEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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 1: Geneseqn1990s:  
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 3: Geneseqm2000s:  
 4: Geneseqm2001ab:  
 5: Geneseqm2002ab:  
 6: Geneseqm2002ab:  
 7: Geneseqm2002ab:  
 8: Geneseqm2003ab:  
 9: Geneseqm2003bs:  
 10: Geneseqm2003cb:  
 11: Geneseqm2004ab:  
 12: Geneseqm2004ab:  
 13: Geneseqm2004ab:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	2836	100.0	2930 3 AAZ50879	Aaz50879 Full length
2	2804.5	100.0	2930 4 ADI10325	Adi10325 Human grot
3	2804.5	98.9	2511 4 ADQ84158	Adq84158 Human tum
4	2804	98.9	2512 4 AAF55900	Aaf55900 Human AST
5	2804	98.9	2626 11 ACN91332	Acn91332 Breast ca

#### ALIGMENTS

RESULT 1  
 AAZ50879 standard; cdna; 2930 BP.  
 ID AAZ50879;  
 XX  
 AC AAZ50879;  
 XX  
 DT 31-MAY-2000 (first entry)

DE

XX

XX

XX

XX

Location/Qualifiers  
 263..1873  
 /\*tag= a  
 /product= "Human GBS toxin receptor protein"

Key  
 CDS

XX

XX

XX

XX

XX

ADL45207 Human ova  
 Adi45207 Marker gene  
 Adi4586 Human NP-  
 Adp5216 PRO polyp

Aak9876 Human ful

Adi12035 Full leng

AAZ50875 Partial h

Aai58115 Human pol

Aaz50876 Sheep GBS

Aad10326 Sheep gro

Aaz50880 Human/she

Az50881 Human/she

Aak79234 Human sod

Aai59001 Human pol

Abq5422 Human ova

Abl90384 Human pol

Aak9301 Human cdn

Adi10328 3', end of

Aak92164 Human

Adi28791 5', end of

Ab103769 Drosophil

Abi18113 Drosophil

Abi07417 Drosophil

Abi103768 Drosophil

Abi13554 Rat DNP

Acf23330 Rat Na-de

Adc15491 Rat DNP

Abi13555 Murine DN

Adc15493 Mouse DNP

Abx13553 Human DNP

Abx13554 Human DNP

Aak2406 Human pol

Abk87049 Human tra

Adg98328 Human tra

Add01393 Human TCH

Add0140 Human TCH

Aai62505 Human tra

Adr08065 Full leng

Add01411 Mouse TCH

Add01422 Mouse TCH

99MO-US016676.







Scoring table:	BLASTM62	Alignments		
Searched:	Gapop 10.0 , Gapext 0.5			
Total number of hits satisfying chosen parameters:	1612378			
Minimum DB seq length: 0				
Maximum DB seq length: 2000000000				
Post-processing: Minimum Match 0%				
Maximum Match 100%				
Listing first 45 summaries				
Database :	UniProt 03: 1: uniprot_sprot: 2: uniprot_trembl: *			
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.				
SUMMARIES				
Result No.	Score	Query Match Length	DB ID	Description
1	2617	100.0	495	1 S175_SHEEP
2	2329	89.0	495	1 S175_RUMAN
3	2236	85.4	495	1 S175_MOUSE
4	1058	40.4	544	2 Q70580
5	1006	38.4	476	2 Q7Q579
6	991.5	37.9	559	2 Q9VYGG7
7	985.5	37.7	502	2 Q9VDDM0
8	979	37.4	589	2 Q8NDX2
9	976	37.3	588	2 Q8K1Q1
10	976	37.3	588	2 Q7TSF2
11	969.5	37.0	601	2 Q8BFU8
12	968.5	37.0	493	1 P02057
13	965	36.9	582	2 Q92057
14	965	36.9	582	2 Q9J112
15	962.5	36.8	582	2 Q8P2U8
16	960	36.7	582	2 Q8BLF2
17	941	36.0	529	1 P1CO_DROME
18	940.5	35.9	576	2 Q6INC8
19	940	35.9	584	2 Q8AW47
20	936	35.8	479	2 Q23514
21	932	35.6	560	2 Q9P2U7
22	927	35.4	560	2 Q62634
23	926	35.4	483	1 P1CO_DROAN
24	923	35.3	560	2 Q7C150
25	899.5	34.4	576	2 Q71513
26	884	33.8	466	2 Q96LH1
27	881	33.7	955	2 Q7Q367
28	874.5	33.4	497	2 Q9Y2CF
29	860	32.9	535	2 Q7PK4
30	859.5	32.8	481	2 Q9VUW8
31	849.5	32.5	533	2 Q7Q1SS

FT	TRANSMEM	201	221	Potential.	RL	Clin. Cancer Res. 7:4182-4194 (2001).
FT	TRANSMEM	228	248	Potential.	RN	[2]
FT	TRANSMEM	289	309	Potential.	RP	SEQUENCE FROM N.A. (ISOFORM 1). FUNCTION, TISSUE SPECIFICITY, VARIANT SD CYS-39, AND VARIANTS ISSD 268-SER-ASN-272 DEL; ARG-183 AND ARG-334.
FT	TRANSMEM	329	349	Potential.	RP	PMID=20047778; PubMed=10581036; DOI=10.1038/70585;
FT	TRANSMEM	366	386	Potential.	RX	Verheijen P.W., Verbeek E., Aula N., Beerns C.E.M.T., Havelaar A.C., Verheijen P.W., Peitonen L., Aula P., Gaijgaard H., van der Spek P.J., Mancini G.M.S.;
FT	TRANSMEM	392	412	Potential.	RA	Joosse M., Peitonen L., Aula N., Beerns C.E.M.T., Havelaar A.C., Verheijen P.W., Verbeek E., Aula N., Beerns C.E.M.T., Havelaar A.C., Mancini G.M.S.;
FT	TRANSMEM	424	444	Potential.	RA	"A new gene, encoding an anion transporter, is mutated in sialic acid storage diseases.";
FT	TRANSMEM	458	478	Potential.	RA	Nat. Genet. 23:462-465 (1999).
SQ	SEQUENCE	495 AA;	5436 MW;	649D7C459B28272 CRC64;	RT	"A new gene, encoding an anion transporter, is mutated in sialic acid storage diseases.";
Qy	Query Match	100.0%;	Score 2617;	DB 1;	RT	storage diseases.";
Qy	Best Local Similarity	100.0%;	Pred. No. 2.8e-183;	Length 495;	RT	storage diseases.";
Db	Matches 495;	Conservative 0;	Nimatches 0;	Indels 0;	RT	storage diseases.";
Db	1	MKSPVSDLAPSDEGEGSDRPLLQAPRABPAPVCCSARYTNLAFLSFFGFVLYSLRVLN	60	;	RL	SEQUENCE FROM N.A. (ISOFORM 2).
Db	1	MKSPVSDLAPSDEGEGSDRPLLQAPRABPAPVCCSARYTNLAFLSFFGFVLYSLRVLN	60	;	RN	PMID=14702039; DOI=10.1038/ng1285;
Qy	61	SVALVDMVDSNTTAKDNRTEYECABHSAPIKVLYNQTCYRWDAAETQWILGSFFYGYI	120	;	RA	Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R., Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H., Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S., Yamamoto J.-I., Saito K., Kawai Y., Nakamura Y., Isono Y., Murakami K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A., Sudo H., Hosoi T., Kaku Y., Kocaira H., Kondo H., Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Ono Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoaka S., Chiba Y., Ishida S., Ono Y., Takiguchi S., Watanabe S., Hotuta T., Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O., Nomura Y., Togiai S., Komai F., Hara R., Takeuchi K., Arita M., Imose N., Murashino K., Yuki Y., Onshima A., Susaki N., Aotsuka S., Yoshihara Y., Matsunaga H., Ichihara T., Shiohata N., Sano S., Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O., Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H., Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B., Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y., Fujimori Y., Komiyama M., Tashiro K., Onishi M., Ohno M., Fujiwara T., Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y., Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikeda Y., Okamoto S., Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeoka K., Senba T., Matsunaga K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M., Togashi T., Oyama M., Hata H., Watanabe M., Konatsu T., Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K., Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R., Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S., "Complete sequencing and characterization of 21,243 full-length human cDNAs.";
Db	121	ITQIPGGYVAISRGKGLLGGIFATAIFLFTPLAADFVGALVALRALEGEGKVYTP	180	;	RT	Nat. Genet. 36:40-45 (2004).
Db	121	ITQIPGGYVAISRGKGLLGGIFATAIFLFTPLAADFVGALVALRALEGEGKVYTP	180	;	RL	SEQUENCE FROM N.A. (ISOFORM 2).
Qy	181	AMHAWKSSWAPPERSKLLISYAGAQLGTIVSPLSLGCVYCYNNWTVYFFGIVGIVW	240	;	RN	TISSUE=Colon;
Db	181	AMHAWKSSWAPPERSKLLISYAGAQLGTIVSPLSLGCVYCYNNWTVYFFGIVGIVW	240	;	RC	PMID=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Qy	241	FILWICLVSDFPTEKTTITPEKEYTLLSLLKNSQKSVWIPMLKSPLWAVVAHPS	300	;	RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
Db	241	FILWICLVSDFPTEKTTITPEKEYTLLSLLKNSQKSVWIPMLKSPLWAVVAHPS	300	;	RA	Alleschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Donald M.P., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loqueland N.A., Peters G.J., Abramson R.D., Mullany S.J., Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Pahey J., Heiton B., Kettman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.D., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimes J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Snailus D.E., Schnerer A., Schein J.E., Jones S.J. M., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
Qy	301	YNTWTFYTLTLLPTMKVEURFNQIENGFLSAVPLGCMILSQAQADNLRAWNFST	360	;	RA	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
Db	301	YNTWTFYTLTLLPTMKVEURFNQIENGFLSAVPLGCMILSQAQADNLRAWNFST	360	;	RN	[5]
Qy	361	LWRRVYESLIGMIGPAFLVAGFICDYSLAVAFLTISTLGGFCSSGSFSINHLDIAPS	420	;	RA	VARIANT SD CYS-39 AND GLU-136, AND VARIANTS ISSD 268-SER-ASN-272 DEL; ARG-183; ARG-334 AND VAL-371.
Db	361	LWRRVYESLIGMIGPAFLVAGFICDYSLAVAFLTISTLGGFCSSGSFSINHLDIAPS	420	;	RP	"Identification of a novel membrane protein, HP59, with therapeutic potential as a target of tumor angiogenesis.";
Qy	421	YAGILGTTNTFATPGMIGPIIARSLTPNTIGEWQTVCIAAAIVNGAIFTLFLARG	480	;	RT	
Db	421	YAGILGTTNTFATPGMIGPIIARSLTPNTIGEWQTVCIAAAIVNGAIFTLFLARG	480	;	RL	
Qy	481	EVQNWAISDQGHRN 495	;	;	RN	
Db	481	EVQNWAISDQGHRN 495	;	;	RC	
RESULT 2	S175_HUMAN	STANDARD; Q9NBR2; Q9J4H0; Created	PRT;	495 AA.	RA	
ID	S175_HUMAN	05-JUL-2004 (Rel. 44, last sequence update)	DT		RA	
AC	Q9NBR2	05-JUL-2004 (Rel. 44, last annotation update)	DT		RA	
DE	Sialin (Solute carrier family 17 member 5) (Sodium/sialic acid cotransporter) (AST) (Membrane glycoprotein HP59).	DE			RA	
DE	Name=SLC17A5; Homo sapiens (Human).	DE			RA	
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.	OS			RA	
OC	NCBI_TaxID=9606;	OC			RA	
RN	[1]	SEQUENCE FROM N.A. (ISOFORM 1). FUNCTION, AND TISSUE SPECIFICITY.	RN		RA	
RP	PubMed=11751519;	RP			RA	
RX	Fu C., Bardhan S., Cetateanu N.D., Wamii B.D., Wang Y., Yan H.-P., Mernaugh R.L., Hellervist C.G., "Identification of a novel membrane protein, HP59, with therapeutic potential as a target of tumor angiogenesis.";	RX			RA	



RESULT 2

Qy 439 IGPPIARSLLPENTIGEWQTVFCIAAAINVFGAIFFTLPAKGEVONWA-TSDHOGH 493  
 Db 422 ISPAVSSYLTPEPGTQEEWQVNLWLTAGLITGALLFSIFFSGEVQWAKITABEGH 477  
 A;Species: Caenorhabditis elegans  
 C;Date: 12-Mar-1993 #sequence\_revision 12-Mar-1993 #text\_change 16-Feb-1997  
 C;Accession: S28286  
 R;Thomas, K.  
 submitted to the EMBL Data Library, December 1992  
 A;Reference number: S28285  
 A;Accession: S28286  
 A;Molecule type: DNA  
 A;Residues: 41-0%; <THO>  
 A;Cross-references: EMBL:Z19153  
 C;Genetics: A;Introns: 50/3; 287/3; 351/3; 412/3  
 C;Keywords: transmembrane protein

Query Match 35.4%; Score 927; DB 2; Length 560;  
 Best Local Similarity 39.4%; Pred. No. 4.4e-66;  
 Matches 184; Conservative 89; Mismatches 168; Indels 26; Gaps 4;

Qy 30 EPAPVCCSA----RYNLAFLSPFGFPFLYSLVRLNVLVALDMDVDSNTAKDNRTSYECA 84  
 Db 48 DPPVVDTCFGFLPERRYTAIMSGIGFCISFGIRCNVGAIVSVNNNSTHRGGHVVQKA 107  
 Qy 85 EHSAPIKVHLNOTSGKRYRNDAEOTGWLICGCSFFYGYIITOIPIGGYVARSRGKLUJLGFIF 144  
 Db 108 Q----FWDNPETVGLHGSFFWNGYVITQIPGGFICRPAANRVEGFAIV 152

Qy 145 ATAIFTLFLPFLAAFGVGALVAIRALEEIGEGGTYPPAHMAMWSSWAPPERSKULSISYA 204  
 Db 153 ATSTUNMLIPSAARVHYGCIVFIRLOGVEGTYPPACHGIWKRWAPPERSRLATTAFC 21.2  
 Qy 205 GAQLGTVVSLPLSGVYCYMMNTWVYFPIFGVGLWFLWICLVSDFPSTKTTKTTPYKE 264  
 Db 213 GSYAVAVVAMPLAGSLVQYSGWSSVFTYGSFGIFFWLFLWVSYEPALHPSTSEEERK 272  
 Qy 265 YILSSLKNOLOSSQSV----PNPMLPLSLPMLAIVWAHFSYNTWTFITLTLPYMEKV 319  
 Db 273 YIEDAIGESAKLANKPTKENTPWRPFTSMVPAVIFCWSWFLYLLISPAYFEV 332  
 Qy 320 LRPNIQENGLFLSAPVYLGWLCLMILSGQADNURARVNNESTUWVRYRFLSLIGMTGPALFL 379  
 Db 333 FGFEISKVLVSALPHLYMIIWVPIGQJADFURSHHMSTVNRLKUNCGGFGMEATL 392  
 Qy 380 VAAGPIGCDYSLSLAVAPLTISTLGGPCCSSGFSINHLDIAPSAGILGLGTNTPATIPGMI 439  
 Db 393 LVGY-SHSKGVAISFLVLAVGFGFATSGENTHNLDAPIRASILMGTSNGVGTLSGMV 451  
 Qy 440 GPITASLTPENTIGEWQTVFLCAAATINFGAIFTFLPAKGEVONWA 486  
 Db 452 CPIIVGAMTKHKTREBWQYFLVYGGVFAASGEKOPWA 498

RESULT 4

Qy 61 TTGMYLSSPFTYPSVNLDSVALVMDNTTAKNRTSYECAHSAPIKVHLNQGKXRYWDAE 106  
 Db 62 LRALEGLGEVTYPPAHMAMWSSWAPPERSKLLSISYAGAQLGRVSPDLSLPGVYCYY-- 120  
 Qy 107 TQGWLIGSPFYGIIITQIPGGYVARSRGKLUJLGFIFATAIFLFLPFLADEFGVGALVA 166  
 Db 121 LRAAIGFLQGATFPAMHTMWSVWGPFLSPLVLTGTVYAGQIGNVIVPLSGPCLCEYGF 180  
 Qy 224 MNWTTVYFPGVFLVWICLIVSDPTPKTCTTPTKSYEYISSLKNOHQSSQ---KS 279  
 Db 181 GGWPSTIPIYGVFGVLUWAWWYVSSDKPAPTHPRTPPEQKIVIAVEASMGKDGTGKVS 240  
 Qy 280 VPWIPMLKSLPLWAIWVVAHFSYNTTFYLTJLPLTYMKSVLRFNQIENGFLSAVYLGCM 339  
 Db 241 TPWIKLTSWAWAAGHAGDQGAYTMVNLSPFLKDVLGLNLSLGAVASIPIYAYF 300  
 Qy 340 LCMILSGQADNLRLARWNFSTLWTRVFSLIGMGPATIYVAAFGIGCDYS-LAVAFLTI 398  
 Db 301 LAINGGGVLLADTLRKSGILSTNTRAAMIVALQGIFIVASGYCGCDDVLYIFITC 360  
 Qy 399 STLGGFCSSGFSGFSGFSGFSGFSGFSGFSGFSGFSGFSGFSGFSGFSGFSGFSGFS 458  
 Db 361 GMAISGLOQYAFVNVNLYIAPPFSGTWVGTTGNTISALAGITSPAVSSYLTPTNGTQEENOM 420  
 Qy 459 VFCIAAAAIVNFGAIFFTLPAKGEVONWA-TSDHOGH 493  
 Db 421 VLWLTAGLITGALLFSIFFSGEVQWAKITABEGH 456

A;Description: is necessary for glutamatergic neurotransmission

RESULT 3

159102 brain specific Na+-dependent inorganic phosphate cotransporter - rat  
 C;Species: Rattus norvegicus (Norway rat)  
 C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
 C;Accession: 159302  
 R;N.; B.; Rose, P.R.; Nadi, N.S.; Paul, S.M.  
 Proc. Natl. Acad. Sci. U.S.A. 91, 5607-5611, 1994  
 A;Title: Cloning and expression of a cDNA encoding a brain-specific Na(+) -dependent inorganic phosphate cotransporter  
 A;Reference number: 159102; MUID:4261635; PMID:202535  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: mRNA  
 A;Residues: 1-563 <LEE>  
 A;Cross-references: UNIPROT:Q97ZN7; EMBL:AF095787; PIDN: AAC64972.1  
 A;Experimental source: strain Bristol N2  
 C;Genetics:  
 A;Gene: eat-4  
 A;Map position: 3  
 C;Function:  
 A;Description: is necessary for glutamatergic neurotransmission

Query Match 31.3%; Score 819; DB 2; Length 563;  
 Best Local Similarity 36.4%; Pred. No. 1.3e-57;  
 Matches 165; Conservative 88; Mismatches 178; Indels 24; Gaps 6;

Qy 36 CSARYNLAFLSPFGFFFLYSLVRLNVLVALDMDVDSNTAKDNRTSYECAHSAPIKVHLN 95  
 Db 53 CRKRWLILATIANGFMISGIRCNFGAAKTHMYKNTD-----PYGKTHM 97

Qy 96 QTGKCKYRWDAAETQGWLGSSFFYGYIITOIPIGGYVARSRGKLUJLGFIFATAIFLFLTPBL 155  
 Db 98 H--BFNTTIDELSMVMESSYFYGYLVTQIPAGFLAAKEPPNKLFQGVGAFNLNLPY 154



121	ITQIPEGGYYASRSRGKKLILLGGIFATAIFLTPLAADFYGALVALRAEGLGEGVTT	180	QY	301	YNTWTFITLTLPLPTYKEVLRFNTIQENGFLSAVPLGWLCLMILSGQADNLRAWNFST
181	AMHAMWSSNAPPERSKLLSISYAGQLGTVSVLPLSGVYCYMMWTVYFFGIVGIIW	240	Db	301	YNTWTFITLTLPLPTYKEVLRFNTIQENGFLSAVPLGWLCLMILSGQADNLRAWNFST
181	AMHAMWSSNAPPERSKLLSISYAGQLGTVSVLPLSGVYCYMMWTVYFFGIVGIIW	240	QY	361	LMVRRFLSIGHTMGPALFLVAAGFIGCDYSLAVAFLTISTLGGFCSGFSINHLDIAPS
241	FILMICLVSPTPETHKTTIYEKEYTLLGGIFATAIFLTPLAADFYGALVALRAEGLGEGVTT	300	Db	361	LMVRRFLSIGHTMGPALFLVAAGFIGCDYSLAVAFLTISTLGGFCSGFSINHLDIAPS
241	FILMICLVSPTPETHKTTIYEKEYTLLGGIFATAIFLTPLAADFYGALVALRAEGLGEGVTT	300	QY	421	YAGILGLITNTATIPGMPIARSLTPTENITGEWQTVFCIAAINVFGAIFTLPAKG
301	YNTWTFITLTLPLPTYKEVLRFNTQENGFLSAVPLGWLCLMILSGQADNLRAWNFST	360	Db	421	YAGILGLITNTATIPGMPIARSLTPTENITGEWQTVFCIAAINVFGAIFTLPAKG
301	YNTWTFITLTLPLPTYKEVLRFNTQENGFLSAVPLGWLCLMILSGQADNLRAWNFST	360	QY	481	EVQNWAI5DHQHGRN 495
361	LMVRRFLSIGHTMGPALFLVAAGFIGCDYSLAVAFLTISTLGGFCSGFSINHLDIAPS	420	Db	481	EVQNWAI5DHQHGRN 495
361	LMVRRFLSIGHTMGPALFLVAAGFIGCDYSLAVAFLTISTLGGFCSGFSINHLDIAPS	420	QY	421	YAGILGLITNTATIPGMPIARSLTPTENITGEWQTVFCIAAINVFGAIFTLPAKG
421	YAGILGLITNTATIPGMPIARSLTPTENITGEWQTVFCIAAINVFGAIFTLPAKG	480	Db	421	YAGILGLITNTATIPGMPIARSLTPTENITGEWQTVFCIAAINVFGAIFTLPAKG
421	YAGILGLITNTATIPGMPIARSLTPTENITGEWQTVFCIAAINVFGAIFTLPAKG	480	QY	481	EVQNWAI5DHQHGRN 495
421	YAGILGLITNTATIPGMPIARSLTPTENITGEWQTVFCIAAINVFGAIFTLPAKG	480	Db	481	EVQNWAI5DHQHGRN 495
RESULT 3					
		US-09-915-181A-7			
		Sequence 7, Application US/09915181A			
		Patent No. US-0020098473A1			
		GENERAL INFORMATION:			
		APPLICANT: EDWARDS, ROBERT			
		APPLICANT: BELLOCCHIO, ELIZABETH			
		APPLICANT: PREMEAU, ROBERT			
		APPLICANT: REIMER, RICHARD			
		TITLE OF INVENTION: NOVEL GIOTAMATE TRANSPORTERS			
		FILE REFERENCE: 305T-926100US			
		CURRENT APPLICATION NUMBER: US/09/915,181A			
		CURRENT FILING DATE: 2002-03-26			
		PRIOR APPLICATION NUMBER: US 60/220,556			
		PRIOR FILING DATE: 2000-07-25			
		NUMBER OF SEQ ID NOS: 11			
		SOFTWARE: PatentIn version 3.0			
		SEQ ID NO 7			
		LENGTH: 495			
		TYPE: PRT			
		ORGANISM: Homo sapiens			
		US-09-915-181A-7			
Query Match 89.0% Score 2329; DB 9; Length 495;					
Best Local Similarity 86.3%; Pred. No. 1..4e-210;					
Matches 427; Conservative 39; Mismatches 29; Indels 0; Gaps 0;					
Qy 1 MKSPVSDLAPSDEEGSDRTPLLQRAPRAEPAVCSARYNLAFLSPFGFFFLYSLRYNL 60					
Db 1 MRSPPVRLARNGEESTDRTPLLPGRAREAPVCARYNLAFLSPFGFFFLYSLRYNL 60					
Qy 61 SVALVDMYDSNTTAKNRTSYCAEHSAPIKVTHNNTGKRYRDAETQWLGSFFYGYI 120					
Db 61 SVALVDMYDSNTTLEDNRTSKACPEHSAPIKVTHNNTGKRYQDAETQWLGSFFYGYI 120					
Qy 121 ITQIPGGVYASGSGGRLLGPFIATAIFLTPLAADDVGVLVALRALEGIGEVGYP 180					
Db 121 ITQIPGGVYASKGGMQLGFLGLTAVLTLFPPIADLGVPVLIVRALEGIGEVGYFP 180					
Qy 181 AMHAMNSWAPPERSKLLSISYAGAOLGTYSPLSGVICYTMNTWTVYFFGIVGIIW 240					
Db 181 AMHAMNSWAPPERSKLLSISYAGAOLGTYSPLSGVICYTMNTWTVYFFGIVGIIW 240					
Qy 241 FILWICLVSPTPETHKTTIYEKEYTLLGGIFATAIFLTPLAADFYGALVALRAEGLGEGVTT					
Db 241 FILWICLVSPTPETHKTTIYEKEYTLLGGIFATAIFLTPLAADFYGALVALRAEGLGEGVTT					
Qy 301 YNTWTFITLTLPLPTYKEVLRFNTIQENGFLSAVPLGWLCLMILSGQADNLRAWNFST					
Db 301 YNTWTFITLTLPLPTYKEVLRFNTIQENGFLSAVPLGWLCLMILSGQADNLRAWNFST					
Qy 361 LMVRRFLSIGHTMGPALFLVAAGFIGCDYSLAVAFLTISTLGGFCSGFSINHLDIAPS					
Db 361 LCVRRLFSIGHTMGPALFLVAAGFIGCDYSLAVAFLTISTLGGFCSGFSINHLDIAPS					
Qy 421 FILMICLVSPTPETHKTTIYEKEYTLLGGIFATAIFLTPLAADFYGALVALRAEGLGEGVTT					
Db 421 FILMICLVSPTPETHKTTIYEKEYTLLGGIFATAIFLTPLAADFYGALVALRAEGLGEGVTT					
Qy 481 EVQNWAI5DHQHGRN 495					
Db 481 EVQNWAI5DHQHGRN 495					
RESULT 2					
		Sequence 4, Application US/10823506			
		Publication No. US20050002331A1			
		GENERAL INFORMATION:			
		APPLICANT: Hellerqvist, Carl			
		APPLICANT: Fu, Changlin			
		TITLE OF INVENTION: GBS Toxin Receptor			
		FILE REFERENCE: CARB-008/01US			
		CURRENT APPLICATION NUMBER: US/10/823,506			
		CURRENT FILING DATE: 2004-04-12			
		PRIOR APPLICATION NUMBER: US/00/359,167			
		PRIOR FILING DATE: 1999-07-21			
		PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60-693,843			
		NUMBER OF SEQ ID NOS: 12			
		SOFTWARE: PatentIn Ver. 2.0			
		SEQ ID NO 4			
		LENGTH: 495			
		TYPE: PRT			
		ORGANISM: Ovis sp.			
Query Match 100.0% Score 2617; DB 17; Length 495;					
Best Local Similarity 100.0%; Pred. No. 9..3e-238; Mismatches 0; Indels 0; Gaps 0;					
Matches 495; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
Qy 1 MKSPVSDLAPSDEEGSDRTPLLQRAPRAEPAVCSARYNLAFLSPFGFFFLYSLRYNL 60					
Db 1 MKSPVSDLAPSDEEGSDRTPLLQRAPRAEPAVCSARYNLAFLSPFGFFFLYSLRYNL 60					
Qy 1 MKSPVSDLAPSDEEGSDRTPLLQRAPRAEPAVCSARYNLAFLSPFGFFFLYSLRYNL 60					
Db 1 MKSPVSDLAPSDEEGSDRTPLLQRAPRAEPAVCSARYNLAFLSPFGFFFLYSLRYNL 60					
Qy 61 SVALVDMYDSNTTAKDNRSTYCAEHSAPIKVHNTQGKRYRDAETQWLGSFFYGYI 120					
Db 61 SVALVDMYDSNTTAKDNRSTYCAEHSAPIKVHNTQGKRYRDAETQWLGSFFYGYI 120					
Qy 121 ITQIPEGGYYASRSRGKKLILLGGIFATAIFLTPLAADFYGALVALRAEGLGEGVTT					
Db 121 ITQIPEGGYYASRSRGKKLILLGGIFATAIFLTPLAADFYGALVALRAEGLGEGVTT					
Qy 121 ITQIPEGGYYASRSRGKKLILLGGIFATAIFLTPLAADFYGALVALRAEGLGEGVTT					
Db 121 ITQIPEGGYYASRSRGKKLILLGGIFATAIFLTPLAADFYGALVALRAEGLGEGVTT					
Qy 181 AMHAMWSSNAPPERSKLLSISYAGQLGTVSVLPLSGVYCYMMWTVYFFGIVGIIW					
Db 181 AMHAMWSSNAPPERSKLLSISYAGQLGTVSVLPLSGVYCYMMWTVYFFGIVGIIW					
Qy 181 AMHAMWSSNAPPERSKLLSISYAGQLGTVSVLPLSGVYCYMMWTVYFFGIVGIIW					
Db 181 AMHAMWSSNAPPERSKLLSISYAGQLGTVSVLPLSGVYCYMMWTVYFFGIVGIIW					
Qy 241 FILMICLVSPTPETHKTTIYEKEYTLLGGIFATAIFLTPLAADFYGALVALRAEGLGEGVTT					
Db 241 FILMICLVSPTPETHKTTIYEKEYTLLGGIFATAIFLTPLAADFYGALVALRAEGLGEGVTT					
Qy 241 FILMICLVSPTPETHKTTIYEKEYTLLGGIFATAIFLTPLAADFYGALVALRAEGLGEGVTT					
Db 241 FILMICLVSPTPETHKTTIYEKEYTLLGGIFATAIFLTPLAADFYGALVALRAEGLGEGVTT					





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OM protein - protein search, using sw model

Run on: July 9, 2005, 05:11:02 ; Search time 108.026 Seconds

(without alignments)

1772.222 Million cell updates/sec

Title: US-09-776-865-4

Perfect score: 2617

Sequence: 1 MKSPVSDLAPSDBEGSDRT.....LPAKGEVQNWAIISDHQGHRN 495

Scoring table: BLOSUM62

Gapop 1.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

- 1: geneseqP1980s:\*
- 2: geneseqP1908s:\*
- 3: geneseqP2000s:\*
- 4: geneseqP2001s:\*
- 5: geneseqP2002s:\*
- 6: geneseqP2003as:\*
- 7: geneseqP2003bs:\*
- 8: geneseqP2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	2617	100.0	495	Aay45088 Sheep GBS
2	2617	100.0	495	Aae06519 Sheep gro
3	2329	89.0	495	AY45087 Partrial h
4	2329	89.0	495	Aab65967 Human AST
5	2329	89.0	495	ADJ75516 Marker ge
6	2329	89.0	495	Adi14587 Human NF-
7	2329	89.0	495	ADP25217 PRO polyp
8	2329	89.0	536	Aay45089 Human GBS
9	2329	89.0	536	Aab06518 Human gro
10	2322	88.7	495	Aam38959 Human pol
11	1702	65.0	495	Aay45090 Human/she
12	1544	59.0	314	AAG65238 Human sod
13	13866	53.0	284	Abp41345 Human ova
14	13188	50.4	272	Abb61975 Human pol
15	1232	47.1	277	Aam93914 Human pol
16	1232	47.1	277	Adi32036 Human pro
17	1217	46.5	309	AAM40745 Human pol
18	991.5	37.9	559	Abb58701 Drosophili
19	985.5	37.7	502	Abb65873 Drosophili
20	985.5	37.7	502	Abb60525 Drosophili
21	979	37.4	589	Aau93329 Human tra
22	979	37.4	589	Aao30994 Human tra
23	979	37.4	589	Add01392 Human TCH
24	979	37.4	589	ADG88329 Human tra
25	979	37.4	589	ADR10021 Human pol

#### ALIGNMENTS

RESULT 1  
ID AAY45088

XX standard, protein, 495 AA.  
ID AAY45088;

XX (first entry)

XX Sheep GBS toxin receptor (SP55).

XX Sheep GBS toxin receptor; group B beta-haemolytic streptococci; SP55; patho logical vascularisation; cancer metastases; angiogenesis; sheep; neovascularisation; reperfusion injury; scarring; keloid; chronic inflammation; rheumatoid arthritis; psoriasis; neural injury; endothelial cell proliferation; antibacterial; anticancer; anti-angiogenic; anti-inflammatory; anti-arthritic; anti-psoriatic.

OS Orvis sp.  
XX

XX Key

XX Peptide

XX FT

XX FT

XX Peptide

XX FT

XX OS

XX XX

FT Modified-site 423. .428  
 FT /label= "Predicted myristylation site"  
 FT 73. .75  
 FT /label= "Predicted phosphorylation site"  
 FT 77. .80  
 FT /label= "Predicted phosphorylation site"  
 FT 79. .82  
 FT /label= "Asn is N-glycosylated"  
 FT 95. .98  
 FT /label= "Predicted phosphorylation site"  
 FT 97. .100  
 FT /note= "Asn is N-glycosylated"  
 FT 97. .99  
 FT /label= "Putative amidation site"  
 FT 126. .131  
 FT /note= "Predicted myristylation site"  
 FT 135. .157  
 FT /note= "Outer boundary of transmembrane domain"  
 FT 137. .153  
 FT /note= "Inner boundary of transmembrane domain"  
 FT 142. .147  
 FT /note= "Predicted myristylation site"  
 FT 162. .167  
 FT /note= "Predicted myristylation site"  
 FT 172. .177  
 FT /note= "Predicted myristylation site"  
 FT 205. .210  
 FT /note= "Predicted myristylation site"  
 FT 209. .214  
 FT /note= "Predicted myristylation site"  
 FT 225. .228  
 FT /note= "Asn is N-glycosylated"  
 FT 226. .252  
 FT /note= "Outer boundary of transmembrane domain"  
 FT 232. .248  
 FT /note= "Inner boundary of transmembrane domain"  
 FT 254. .256  
 FT /label= "PKC phospho site  
 FT /note= "Predicted phosphorylation site"  
 FT 259. .262  
 FT /label= "CK2 phospho site  
 FT /note= "Predicted phosphorylation site"  
 FT 269. .271  
 FT /label= "PKC phospho site  
 FT /note= "Predicted phosphorylation site"  
 FT 276. .278  
 FT /label= "Predicted phosphorylation site"  
 FT 302. .305  
 FT /note= "Asn is N-glycosylated"  
 FT 328. .345  
 FT /note= "Outer boundary of transmembrane domain"  
 FT 328. .344  
 FT /note= "Inner boundary of transmembrane domain"  
 FT 337. .342  
 FT /note= "Predicted myristylation site"  
 FT 357. .360  
 FT /note= "Asn is N-glycosylated"  
 FT 365. .389  
 FT /note= "Outer boundary of transmembrane domain"  
 FT 369. .385  
 FT /note= "Inner boundary of transmembrane domain"  
 FT 386. .391  
 FT /note= "Predicted myristylation site"  
 FT 390. .407  
 FT /note= "Outer boundary of transmembrane domain"  
 FT 390. .406  
 FT /note= "Inner boundary of transmembrane domain"  
 FT 403. .408  
 FT /note= "Predicted myristylation site"

FT Modified-site 423. .428  
 FT /note= "Predicted myristylation site"  
 FT 427. .432  
 FT /note= "Predicted myristylation site"  
 FT 452. .455  
 FT /label= "CK2 phospho site  
 FT /note= "Predicted phosphorylation site"  
 FT 456. .479  
 FT /note= "Outer boundary of transmembrane domain"  
 FT 458. .474  
 FT /note= "Inner boundary of transmembrane domain"  
 XX WO200005375-A1.  
 PD 03-FEB-2000.  
 XX 22-JUL-1999; 99WO-US016676.  
 XX 22-JUL-1998; 98US-0093843P.  
 XX (UVA-) UNIV VANDERBILT.  
 PA  
 XX  
 PI Hellerqvist CG, Fu C;  
 XX  
 PR WPI: 2000-205377/18.  
 DR N-PSDB; AAZ50876.  
 XX  
 PR New polynucleotide encoding mammalian receptor for streptococcus toxin,  
 useful for diagnosis and treatment of, e.g. pneumonia in neonates.  
 PS  
 XX  
 PS  
 XX  
 CC The present sequence is sheep GBS (group B beta-haemolytic streptococci)  
 CC toxin receptor (SP55). Sheep GBS toxin receptor is an integral protein  
 CC with seven transmembrane domains. Expression vectors comprising the  
 CC coding region can be transformed into host cells to express GBS toxin  
 CC receptor and its fragments. Detecting the receptor in tissues is used to  
 CC diagnose pathological vascularisation, e.g. for detecting cancer  
 CC metastases. GBS toxin receptors are useful for treating conditions  
 CC associated with pathological angiogenesis or neovascularisation  
 CC (specifically cancer, reperfusion injury, scarring during wound healing,  
 CC keloids, chronic inflammation (rheumatoid arthritis or psoriasis) or  
 CC neural injury), and to raise specific antibodies used for treating early  
 CC onset disease. Inhibitors of this receptor are useful for treating  
 CC pathological or hypoxia-induced endothelial cell proliferation and  
 CC migration  
 XX  
 SQ Sequence 495 AA;  
 SQ  
 Query Match 100.0%; Score 2617; DB 3; Length 495;  
 Best Local Similarity 100.0%; Pred. No. 1.8e-273;  
 Matches 495; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKSPVSDLAPSDEEGSDRTPLQRAAPEPAPVCCSARYNLAFLSPRGFPVLYSLRNL 60  
 DB 61 SVALIVMDYDSNTIAKDNRTSYCAEHASAPIKVLYHNOTCKKYRDAETQGWIGSFFFGYI 120  
 QY 1 MKSPVSDLAPSDEEGSDRTPLQRAAPEPAPVCCSARYNLAFLSPRGFPVLYSLRNL 60  
 DB 61 SVALIVMDYDSNTIAKDNRTSYCAEHASAPIKVLYHNOTCKKYRDAETQGWIGSFFFGYI 120  
 QY 121 ITQIPGG3YVARSRGKLLGFGIFATAIITLFTPLAADFVGALVRALEGEGEGTYP 180  
 DB 121 ITQIPGG3YVARSRGKLLGFGIFATAIITLFTPLAADFVGALVRALEGEGEGTYP 180  
 QY 61 SVALIVMDYDSNTIAKDNRTSYCAEHASAPIKVLYHNOTCKKYRDAETQGWIGSFFFGYI 120  
 DB 61 SVALIVMDYDSNTIAKDNRTSYCAEHASAPIKVLYHNOTCKKYRDAETQGWIGSFFFGYI 120  
 QY 121 ITQIPGG3YVARSRGKLLGFGIFATAIITLFTPLAADFVGALVRALEGEGEGTYP 180  
 DB 121 ITQIPGG3YVARSRGKLLGFGIFATAIITLFTPLAADFVGALVRALEGEGEGTYP 180  
 QY 181 AMFAMWSSWAPPLERSKLSISYAGQLGTVSLPLSGVIVCYMNTVYFFGIGIVIW 240  
 DB 181 AMFAMWSSWAPPLERSKLSISYAGQLGTVSLPLSGVIVCYMNTVYFFGIGIVIW 240  
 QY 241 FILWICLVSDFPETHKTTIPYKEYIILSLKQHQLSSRSVPWITPMLKSLPLWAVVAFS 300  
 DB 241 FILWICLVSDFPETHKTTIPYKEYIILSLKQHQLSSRSVPWITPMLKSLPLWAVVAFS 300

Result No.	Score	Query	Match	Length	DB	ID	Description
1	2621	92.4	495	1	'S175_HUMAN		09nz42 homo sapien
2	2329	82.1	495	1	'S175_SHEEP		Q9mza1 ovis aries
3	2298	81.0	495	1	'S175_MOUSE		Q8bn82 mus musculus
4	1051	37.1	544	2	Q70580		Q7q590 anophelis g
5	996.5	35.1	559	2	Q9VY77		Q9vy77 drosophila
6	992	35.0	502	2	Q9VDM0		Q9vdn0 drosophila
7	991	34.9	476	2	Q70579		Q7q579 anophelis g
8	987	34.8	493	1	YLD2_CAEEL		Q03567 caenorhabdi
9	970	34.2	582	2	Q920B7		Q920b77 mus musculus
10	970	34.2	582	2	Q9J112		Q9j112 rattus norvegicus
11	966.5	34.1	584	2	Q8AW47		Q8aw47 brachydanio
12	965.5	34.0	582	2	Q9P2U8		Q9p2u8 homo sapien
13	965	34.0	582	2	Q9BLE7		Q8ble7 mus musculus
14	955	33.7	589	2	Q8NDX2		Q8ndx2 homo sapien
15	954.5	33.7	588	2	Q8K1Q1		Q8k1q1 rattus norvegicus
16	954.5	33.7	588	2	Q7SP2		Q7sp2 rattus norvegicus
17	946.5	33.4	479	2	Q23514		Q23514 caenorhabditis elegans
18	945	33.3	601	2	Q8BFU8		Q8bfu8 mus musculus
19	941	33.2	560	2	Q9P2U7		Q9p2u7 homo sapien
20	939.5	33.1	576	2	Q6INC8		Q6inc8 xenopus laevis
21	936	33.0	560	2	Q62634		Q62634 rattus norvegicus
22	932	32.9	560	2	Q6PCD0		Q6pcd0 homo sapien
23	928.5	32.7	529	1	ETICO_DROME		Q9v785 drosophila
24	917	32.3	483	1	ETICO_DROAN		061169 drosophila
25	913	32.2	576	2	Q715L3		Q715l3 xenopus laevis
26	905	31.9	955	2	Q7Q367		Q7q367 anophelis gambiae
27	895	31.6	466	2	Q96LH1		Q96lh1 homo sapien
28	889.5	31.4	533	2	Q9Y2C5		Q9y2c5 anophelis gambiae
29	876	30.9	497	2	Q7PKW4		Q7pkw4 homo sapien
30	870.5	30.7	535	2	Q9W4G7		Q9w4g7 drosophila
31	856	30.6	493	2			

RESULT 1							
ID	S175_HUMAN	STANDARD		PRT:	495 AA.		
AC	Q9NFR2; Q8NBRS; Q9NGHO;						
DT	05-JUL-2004 (Rel. 44, Created)						
DT	05-JUL-2004 (Rel. 44, Last sequence update)						
DT	05-JUL-2004 (Rel. 44, Last annotation update)						
DE	Sialin (Solute carrier family 17 member 5) (Sodium/sialic acid cotransporter) (AST) (Membrane glycoprotein HP59).						
DB	NCBI_TaxID=9606;						
GN	Name=SLC17A5;						
OS	Homo sapiens (Human).						
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.						
OX							
RN	SEQUENCE FROM N.A. (ISOFORM 1), FUNCTION, TISSUE SPECIFICITY.						
RP	SEQUENCE FROM N.A. (ISOFORM 1), FUNCTION, TISSUE SPECIFICITY.						
RX	PubMed=11751519;						
RX	Fu C., Bardhan S., Cetateanu N.D., Wanil B.D., Wang Y., Yan H.-P., Shi E., Carter C., Venkov C., Yakes F.M., Page D.L., Lloyd R.S., Mernaugh R.L., Heilekrist C.G.,						
RA	"Identification of a novel membrane protein, HP59, with therapeutic potential as a target of tumor angiogenesis.";						
[1]	Clin. Cancer Res. 7:4162-4194 (2001).						
RN	SEQUENCE FROM N.A. (ISOFORM 1), FUNCTION, TISSUE SPECIFICITY, VARIANT SD CYS-39, AND VARIANTS ISSD 268-SER-ASN-272 DEL; ARG-183 AND ARG-334.						
RP	RP MEDLINE=20047778; PubMed=10581036; DOI=10.1038/70585;						
RX	Verheijen F.W., Verbeek E., Aula N., Beerens C.E.M.T., Havelaar A.C., Joosse M., Peltonen L., Aula P., Galjgaard H., van der Spek P.J., Mancini G.M.S.;						
RA	"A new gene, encoding an anion transporter, is mutated in sialic acid storage disease 9";						
RT	Nat. Genet. 23:4462-4465 (1999).						
RL	SEQUENCE FROM N.A. (ISOFORM 2).						
RX	PubMed=14702039; DOI=10.1038/ng1285;						
RA	Ota T., Suzuki Y., Nishikawa T., Otsubi T., Sugiyama T., Irie R., Wakamatsu A., Hayashi K., Nishio K., Sato K., Makita H., Sekine M., Obayashi M., Nishi T., Shishibahara T., Tanaka T., Ishii S., Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K., Murakami K., Yasuda T., Waga S., Sugawara M., Shiratori A., Sudo H., Hosoi T., Kato Y., Kodaира H., Kondo H., Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y., Abe K., Kamihara K., Katsuma N., Sato K., Arita M., Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K., Tanai H., Kimata M., Watanabe M., Hiroaka S., Chiba Y., Ishida S., Ono Y., Takiguchi S., Yosida M., Hotuta T., Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanabe T.-O., Nomura Y., Togiai S., Komai F., Hara R., Takeuchi K., Arita M., Imbe N., Matsunawa H., Yuki H., Ohshima A., Sasaki N., Mizoguchi H., Yoshioka Y., Momiya H., Ichihara T., Shiohama N., Sano S., Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O., Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,						

## ALIGNMENTS

## SUMMARIES

## Post-processing:

## Database:

## Perfect score:

## Sequence:

## Scoring table:

## Searched:

## Total number of hits satisfying chosen parameters:

1612378 seqs, 512079187 residues

1612378

## Minimum DB seq length: 0

## Maximum DB seq length: 2000000000

## Post-processing: Minimum Match 0%

## Maximum Match 100%

## Listing First 45 summaries

## UniProt 03:\*

## 1: uniprot\_sprot:\*

## 2: uniprot\_trembl:\*

## Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution, and is derived by analysis of the total score distribution.

## SUMMARIES

## %

## Score

## Match

## Length

## DB

## ID

## Description





RESULT 2

Qy 467 LGITNTPATIPGMVCPVIAKSLLTPDNTVGEWQTVPIAAINVGAIFFLPAKEGEVQNW 526  
 Db 409 MGTGNTISALAGITISPAVSSYLTPTNGTQBEWQMLWLTAGLTIGALLSIFASGEVQFW 468  
 Qy 527 A-LNDHGH 534  
 Db 469 AKLTABEGH 477

hypothetical protein C3AC10\_2 - *Caenorhabditis elegans*  
 C;Species: *Caenorhabditis elegans*  
 C;Date: 12-Mar-1993 #sequence revision 12-Mar-1993 #text\_change 16-Feb-1997  
 C;Accession: S28286  
 R;Thomas, K.  
 submitted to the ENBL Data Library, December 1992  
 A;Reference number: S28285  
 A;Accession: S28286  
 A;Molecule type: DNA  
 A;Residues: 1-472 <THO>  
 A;Cross-references: EMBL:Z19153  
 C;Genetics:  
 A;Introns: 50/3; 287/3; 351/3; 412/3  
 C;Keywords: transmembrane protein

Query Match 34.1%; Score 967; DB 2; Length 472;  
 Best Local Similarity 41.0%; Pred. No. 1.6e-68;  
 Matches 18; Conservative 8; Mismatches 10; Gaps 5;

Qy 88 FFGPPFVYALRVNLSQLVMDNSNTLEDNRTSKACPEHSAPIKVHHNQTYQWDAE 147  
 Db 2 FFGCLVTVNRTNMSFAVVCVNENKTDTGVEKVYKSRGKEMTPVTESSNSVIG-EFDWDIQ 60  
 Qy 148 TQGWILGSPFTGYYITQIOPGYYVASKIGKMLLGFGLGTTAVLTLFPTIAADLGVGPLTV 207  
 Db 61 TTGMYLSSPFTGYYGQSQIIGHLASRYGRVVFVFTGSLALLTINPVAARTSEYALI 120  
 Qy 208 LRAEGLGEVTFPAMHMMSSWAPLERSKLLSISYAGQLGTVTSLPSPGICYY-- 264  
 Db 121 LRAAGFLQGATFPAMHMMWSVGPPLLESLVLTGTYAGQGINVTVLPPSGFCEYGD 180  
 Qy 265 MNWTVYFEGTIGFWLWLNQSDTPQKHKLISHYKEYTLSSRNQLSSQ---KS 320  
 Db 181 CGWPSIYIIGVFGVLWNTAWWVYVSSDKPATHPRITPEEKYQTVTAAEAMGKDTGKVP 240  
 Qy 321 VPWPLIKSPPLWAIWVAAHHSYNTWPTYLTLPPYMKETLRFNQENGFLSSEPYLGW 380  
 Db 241 TPWIKLTSPPAVWAGHAGDWTGAYTMVSLPSFLQWGLNLISSLGAVASIPYAYF 300

Qy 381 LCMILSQAADDNLRAKWNFSPLCVRISIISGMICPAVFLVAAFTIGCDYS-LAVAFLTI 439  
 Db 301 LAINAGGLVADTLRSGILSTLNTRAAMLVALIQCQGIFLVAISGVCGCGDVLVIFTC 360  
 Qy 440 STTLLGGFCSSGSFSINHLDIAAPSAYGTLGTTNTFATIPGMVGPVIAKSLLTPDNTVGEWQT 499  
 Db 361 GMAISGLQYGFVNVYLEIAPPFSGTMGPGNTISALAGITISPAVSSYLTPTNGTOBEMW 420  
 Qy 500 VFIYAAAINVGAIFPTLPAKEGEVQNWIA-LNDHGH 534  
 Db 421 VMLTAGLITGALLSIFASGEVQFWKLTAEEGH 456

RESULT 3

I59302 brain specific Na+-dependent inorganic phosphate cotransporter - rat  
 C;Species: *Rattus norvegicus* (Norway rat)  
 C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
 C;Accession: I59302  
 R;Ni, B.; Roseck, P.R.; Nadi, N.S.; Paul, S.M.  
 Proc. Natl. Acad. Sci. U.S.A. 91, 5607-5611, 1994  
 A;Title: Cloning and expression of a cDNA encoding a brain-specific Na(+) -dependent inos

A;Reference number: I59302; MUID:94261635; PMID:8202535  
 A;Accession: I59302  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: mRNA  
 A;Residues: 1-560 <RES>  
 A;Cross-references: UNIPROT:Q62634; EMBL:U07609; NID:9507414; PID:950741; PID:950741  

Query Match 33.0%; Score 936; DB 2; Length 560;  
 Best Local Similarity 33.0%; Pred. No. 5.5e-6;  
 Matches 190; Conservative 91; Mismatches 168; Indels 38; Gaps 7;

Qy 53 DGBBESTDRD--PLP--GAPRAEAAAPVCSARVSYNIALAIAFFGFIYVYALRVNLSVAL 105  
 Db 38 DGRPVTTHTRDPPVDTCTCFLPR-----RYIAIMSGLFCISFGIRCNLGVAI 87

Qy 106 VDMYDNTSNTLEDNRTSKACPEHSAPIKVHNNTCTKQYQDAETGWLGSFFTCYIITQI 165  
 Db 88 VSMVNNTT-----HRGGHVVYVKAQ-----RYIAIMSGLFCISFGIRCNLGVAI 132

Qy 166 PGGYVASKIGKMLLGFGLGTTAVLTLFPTIAADLGVGPLIVRALEGEGTGFPPAMHA 225  
 Db 133 PGGFCICQKPAANRVEFGALVATSTLNMLPSAARVHYGCIVTFRILQHVEGTVYPACHG 192

Qy 226 MWSNAPPLERSKLLSISYAGQLGTVTSLPLSGLICYYMNNTWTFVYFPGTIGFWFLW 285  
 Db 193 IWSKRNAPPPLERSRLATATFCGTSYAVAVYAMPLAGVLYQSGWSSVYVYGSFG1FWLFW 252

Qy 286 IWLVSDTPQKHKRATSHYECYIISLRLNGLSSRSKV-----PWPPLKSLPLWAVIAVHF 340  
 Db 253 LLVSVSPALHPSPISSEBERYIEAGBALKNPVTKENTPWERFPTSMVPAVIAVANF 312

Qy 341 SYNTTPTYLTLLPTYMKELRNVQENGFLSSPLYPSWLCMILSGLQADNLRAKWNFS 400  
 Db 313 CRSTWFLYLISQPAYFEEVFGFELISKVGLSALPHLMTIIVPIGQIADFLFRSHIMS 372

Qy 401 TICVRRIFSLIGMTGPAVLVAAGFPGCDYSLAVAFLTISTLUGFCSCSGFSINHLDIAP 460  
 Db 373 TTNVYKLMNCGGFGMELATLUVVGY-SHSKGVAISFLVLAVGFSGEAISGENYNHLDIAP 431

Qy 461 SYAGLGLITNTFATIPGMVGPVIAKSLLTPDNTVGEWQTFTVYIAAATNFGAIFPTFLFK 520  
 Db 432 RYASTLGMISNGVGTLSGMVCPiIYVGMFTKHTREEWQTVFLIASLHVYGGVIFYGVFAS 491

RESULT 4

Qy 521 GEVQWNA 527  
 Db 492 GEKQEWNA 498

A;Alternate names: sodium/phosphate cotransporter  
 C;Species: Oryctolagus cuniculus (domestic rabbit)  
 C;Date: 21-Jul-1995 #sequence\_revision 21-Jul-1995 #text\_change 09-Jul-2004  
 C;Accession: A56410; S27951  
 R;Warner, A.; Moore, M.L.; Mantei, N.; Biber, J.; Semenza, G.; Murer, H.  
 Proc. Natl. Acad. Sci. U.S.A. 88, 9608-9612, 1991  
 A;Title: Cloning and expression of cDNA for a Na/P-i cotransport system of kidney cortex.  
 A;Accession: A56410; MUID:9205214; PMID:1946375  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-465 <RES>  
 A;Keywords: kidney; transmembrane protein

Query Match 29.0%; Score 822.5; DB 2; Length 465;  
 Best Local Similarity 37.4%; Pred. No. 4e-57;  
 Matches 172; Conservative 83; Mismatches 196; Indels 9; Gaps 4;

Qy 74 PVCCCSARVSYNIALAIAFFGFIYVYALRVNLSVALVDMDSNTTLEDNRTSKACPEHSAPIKV 133  
 Db 11 PCFCFSRYYLALPNCFCNIVIAORMCLSLTMVAMV-NNTNLHGS-----PNTSAEKR1 63

SUMMARIES									
Query	Match	Length	DB	ID	Description	Score	2836;	DB 9;	Length 536;
1	2836	100.0	536	9	US-09-776-865-2	Sequence 2, Appli	100 0%	Pred. No. 3.6e-249;	
2	2836	100.0	536	17	US-10-823-506-8	Sequence 8, Appli	100 0%	Mismatches 0;	
3	2621	92.4	495	9	US-09-915-18A-7	Sequence 7, Appli	100 0%	Indels 0;	
4	2621	92.4	495	16	US-10-755-889-588	Sequence 588, Appli	100 0%	Gaps 0;	
5	2621	92.4	495	17	US-10-823-506-2	Sequence 2, Appli	100 0%		
6	2329	82.1	495	9	US-09-776-865-4	Sequence 4, Appli	100 0%		
7	2329	82.1	495	17	US-10-823-506-4	Sequence 4, Appli	100 0%		
8	1698	59.9	495	17	US-10-823-506-10	Sequence 10, Appli	100 0%		
9	1698	59.9	495	17	US-10-823-506-12	Sequence 12, Appli	100 0%		
10	1521	53.6	284	15	US-10-264-049-2477	Sequence 2477, Appli	100 0%		
11	1451	53.6	272	15	US-10-264-237-2357	Sequence 2357, Appli	100 0%		

121 SKACPEHSAPIKVHINOTGKRYQWDAETQWILGSFFYGYITIQPGYVASKIGGKML 180  
 181 GFGILGTAVITLFTP1AADDVGPLIVLRALEGLEGGVTPAMHAWSSWAPPERSKLL 240  
 Db 181 GFGILGTAVITLFTP1AADDVGPLIVLRALEGLEGGVTPAMHAWSSWAPPERSKLL 240  
 241 SISYAGAQLGVTVISLPLSGICYYMWNTYVYFFSTGIFTYFWFLWILWYSDTPKHKRIS 300  
 Qy 241 SISYAGAQLGVTVISLPLSGICYYMWNTYVYFFSTGIFTYFWFLWILWYSDTPKHKRIS 300  
 Db 241 SISYAGAQLGVTVISLPLSGICYYMWNTYVYFFSTGIFTYFWFLWILWYSDTPKHKRIS 300  
 301 HYEKEYILSSLRNQLSQKSVWPWVPIKSLPLWIAVVAHFSYNNTPYTYLTLPLTYMKI 360  
 Qy 301 HYEKEYILSSLRNQLSQKSVWPWVPIKSLPLWIAVVAHFSYNNTPYTYLTLPLTYMKI 360  
 Db 361 LRNFVQENGFLSSLPYLGSLCMILSGQADNLRAKWNFSTLCVRRIFSLIGMIGPAVPL 420  
 Qy 361 LRNFVQENGFLSSLPYLGSLCMILSGQADNLRAKWNFSTLCVRRIFSLIGMIGPAVPL 420  
 Db 361 LRNFVQENGFLSSLPYLGSLCMILSGQADNLRAKWNFSTLCVRRIFSLIGMIGPAVPL 420  
 Qy 421 VAAGFIGCDYSLAVAFLTISSTLGFCSSGFSINHLDAPSAGILGTTNTFATIPGMV 480  
 Db 421 VAAGFIGCDYSLAVAFLTISSTLGFCSSGFSINHLDAPSAGILGTTNTFATIPGMV 480  
 481 GPIVAKSLTPDNTVGEWQTFYIAAANVFGAIPTFLFAKEVONWALNDHHGHRH 536  
 Qy 481 GPIVAKSLTPDNTVGEWQTFYIAAANVFGAIPTFLFAKEVONWALNDHHGHRH 536  
 Db 481 GPIVAKSLTPDNTVGEWQTFYIAAANVFGAIPTFLFAKEVONWALNDHHGHRH 536  
 Qy 481 GPIVAKSLTPDNTVGEWQTFYIAAANVFGAIPTFLFAKEVONWALNDHHGHRH 536  
 Db 481 GPIVAKSLTPDNTVGEWQTFYIAAANVFGAIPTFLFAKEVONWALNDHHGHRH 536

RESULT 3  
 US-09-915-181A-7  
 ; Sequence 7, Application US/09915181A  
 ; Patent No. US20020098473A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: EDWARDS, ROBERT  
 ; BELLOCCHIO, ELIZABETH  
 ; APPLICANT: PREMEAU, ROBERT  
 ; APPLICANT: REIMER, RICHARD  
 ; TITLE OF INVENTION: NOVEL GLUTAMATE TRANSPORTERS  
 ; FILE REFERENCE: 305T-932610US  
 ; CURRENT APPLICATION NUMBER: US/09/915,181A  
 ; CURRENT FILING DATE: 2002-03-26  
 ; PRIOR APPLICATION NUMBER: US 60/220,556  
 ; PRIOR FILING DATE: 2000-07-25  
 ; NUMBER OF SEQ ID NOS: 11  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 7  
 ; LENGTH: 495  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-09-915-181A-7

Query Match 92.4%; Score 2621; DB 9; Length 495;  
 Best Local Similarity 100.0%; Pred. No. 1 2e-229;  
 Matches 495; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

42 MRSPPRDLARNGEBSTDTPPLGAPRAEAAAPVCCSARYNLLAFFFIVYALRVLN 101  
 1 MRSPPRDLARNGEBSTDTPPLGAPRAEAAAPVCCSARYNLLAFFFIVYALRVLN 60

Qy 102 SVALVMDVDSNTTLEDNRTSKACPEHSAPIKVHINOTGKRYQWDAETQWILGSFFYGYI 161  
 Db 61 SVALVMDVDSNTTLEDNRTSKACPEHSAPIKVHINOTGKRYQWDAETQWILGSFFYGYI 120

1 MAAGANTPPREVQPARPGGPELSGRSLLCQAVASTPARYVMSPRVDLARNGEBESTR 60  
 1 MAAGANTPPREVQPARPGGPELSGRSLLCQAVASTPARYVMSPRVDLARNGEBESTR 60  
 LENGTH: 536  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-823-506-8

Query Match 100.0%; Score 2836; DB 17; Length 536;  
 Best Local Similarity 100.0%; Pred. No. 3.6e-249;  
 Matches 536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

61 TPLPGAPRAEAAAPVCCSARYNLLAFFFIVYALRVLNSVALVDYMDNTTLEDNRT 120  
 61 TPLPGAPRAEAAAPVCCSARYNLLAFFFIVYALRVLNSVALVDYMDNTTLEDNRT 120  
 121 SKACPEHSAPIKVHINOTGKRYQWDAETQWILGSFFYGYITIQPGYVASKIGGKML 180  
 121 SKACPEHSAPIKVHINOTGKRYQWDAETQWILGSFFYGYITIQPGYVASKIGGKML 180  
 Db 121 SKACPEHSAPIKVHINOTGKRYQWDAETQWILGSFFYGYITIQPGYVASKIGGKML 180  
 181 GFGILGTAVITLFTP1AADDVGPLIVLRALEGLEGGVTPAMHAWSSWAPPERSKLL 240  
 Qy 181 GFGILGTAVITLFTP1AADDVGPLIVLRALEGLEGGVTPAMHAWSSWAPPERSKLL 240  
 Db 181 GFGILGTAVITLFTP1AADDVGPLIVLRALEGLEGGVTPAMHAWSSWAPPERSKLL 240  
 Qy 241 SISYAGAQLGVTVISLPLSGICYYMWNTYVYFFSTGIFTYFWFLWILWYSDTPKHKRIS 300  
 Db 241 SISYAGAQLGVTVISLPLSGICYYMWNTYVYFFSTGIFTYFWFLWILWYSDTPKHKRIS 300

402 LCVERIFSLIGMIGPAVFLVAVGFIGCDYSLAVFLTISTLGGFCSSFSINHLDIAFS 461  
 361 LCVRRIFSLIGMIGPAVFLVAVGFIGCDYSLAVFLTISTLGGFCSSFSINHLDIAFS 420

GenCore version 5.1.6  
(c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 9, 2005, 06:00:41 ; Search time 30.6731 Seconds  
(without alignments)  
1304.461 Million cell updates/sec

Title: US-09-776-865-2

Perfect score: 2836

Sequence: 1 MAAGATTPRPPVQPARPGGP.....LFAKGEVQNVNALNDIGHGRH 536

Scoring table: BLOSUM62

Gappen 0.0 , Gapext 0.5

Searched:

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*

1: /cgna\_6/\_ptodata/1/iaa/5a\_COMB.pep \*  
2: /cgna\_6/\_ptodata/1/iaa/5b\_COMB.pep \*  
3: /cgna\_6/\_ptodata/1/iaa/6a\_COMB.pep \*  
4: /cgna\_6/\_ptodata/1/iaa/6b\_COMB.pep \*  
5: /cgna\_6/\_ptodata/1/iaa/70\_COMB.pep \*  
6: /cgna\_6/\_ptodata/1/iaa/backfile1.pep \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	2836	100.0	536	4	US-09-359-167-8	Sequence 8, Appli
2	2804.5	98.9	585	4	US-09-349-016-7705	Sequence 7705, Appli
3	2621	92.4	495	4	US-09-359-167-2	Sequence 2, Appli
4	2621	92.4	495	4	US-09-915-181A-7	Sequence 7, Appli
5	2329	82.1	495	4	US-09-359-167-4	Sequence 4, Appli
6	1698	59.9	495	4	US-09-359-167-10	Sequence 10, Appli
7	1698	59.9	495	4	US-09-359-167-12	Sequence 12, Appli
8	970	34.2	578	4	US-09-740-041-4	Sequence 4, Appli
9	970	34.2	582	4	US-09-915-181A-4	Sequence 4, Appli
10	955	33.7	589	4	US-09-940-041-2	Sequence 2, Appli
11	941	33.2	567	4	US-09-949-016-11354	Sequence 11354, Appli
12	940	33.1	560	1	US-08-647-484-2	Sequence 2, Appli
13	940	33.1	560	1	US-08-647-481-2	Sequence 2, Appli
14	940	33.1	560	1	US-08-430-033A-2	Sequence 2, Appli
15	940	33.1	560	5	FCT US9-05792-2	Sequence 4, Appli
16	936	33.0	560	2	US-08-805-18-4	Sequence 4, Appli
17	936	33.0	560	3	US-09-391-058-4	Sequence 4, Appli
18	936	33.0	560	4	US-09-915-181A-5	Sequence 5, Appli
19	935	33.0	850	4	US-09-915-181A-3	Sequence 3, Appli
20	876	30.9	497	4	US-09-949-016-6616	Sequence 6616, Appli
21	810	28.6	552	4	US-09-270-767-44540	Sequence 45540, Appli
22	808	28.5	563	4	US-09-915-181A-6	Sequence 6, Appli
23	808	28.5	576	3	US-08-864-085-1	Sequence 1, Appli
24	806.5	28.4	465	4	US-09-181-181A-8	Sequence 8, Appli
25	801.5	28.3	467	2	US-08-805-18-3	Sequence 3, Appli
26	801.5	28.3	467	3	US-09-391-058-3	Sequence 3, Appli
27	793	28.0	480	2	US-08-724-394A-9	Sequence 9, Appli

#### ALIGNMENTS

RESULT 1  
US-09-359-167-8  
; Sequence 8, Application US/09359167  
; Patent No. 6803448  
; GENERAL INFORMATION:  
; APPLICANT: Hellqvist, Carl  
; TITLE OF INVENTION: GBS Toxin Receptor  
; FILE REFERENCE: CARB-008/01US  
; CURRENT APPLICATION NUMBER: US/09/359,167  
; CURRENT FILING DATE: 1999-07-21  
; EARLIER APPLICATION NUMBER: 60-693, 843  
; EARLIER FILING DATE: 1998-07-22  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO: 8  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-359-167-8

28	686	24.2	436	4	US-09-949-016-11448
29	686	24.2	470	2	US-08-724-394A-10
30	615.5	21.7	401	2	US-08-805-118-1
31	615.5	21.7	401	3	Sequence 1, Appli
32	592.5	20.9	480	2	US-08-724-394A-11
33	562	19.8	380	4	US-09-949-016-07053
34	453	16.0	460	4	US-09-189-039A-9663
35	45.5	15.7	234	4	US-09-270-767-45527
36	375	13.2	186	4	Sequence 45527, A
37	373	13.2	434	4	Sequence 13633, A
38	370	13.0	470	4	Sequence 6912, Ap
39	369	13.0	439	3	Sequence 14, Appli
40	369	13.0	439	2	Sequence 12, Appli
41	368	13.0	157	4	Sequence 61037, A
42	355.5	12.5	455	4	Sequence 9942, Ap
43	346.5	12.2	459	4	Sequence 10630, A
44	332	11.7	163	4	Sequence 32926, A
45	332	11.7	163	4	Sequence 48143, A

RESULT 2  
US-09-949-016-7705  
Sequence 7705, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CLO01307  
CURRENT APPLICATION NUMBER: US/09/949, 016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: fastSEQ for Windows Version 4.0  
SEQ ID NO: 7705  
LENGTH: 585  
TYPE: PRT  
ORGANISM: Human  
US-09-949-016-7705

Query Match 98.9%; Score 2804.5; DB 4; Length 585;  
Best Local Similarity 95.9%; Pred. No. 2.1e-290; Indels 21; Gaps 1;  
Matches 534; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

Qy 1 MAAGAMT-----: PPRVQPARPGGFGLSGRPSLQVASTPARY 39  
Db 29 MAAGAESARPPLGGTAGTRGRGAVSSPPRVPQPARPGGFGLSGRPSLQVASTPARY 88  
Qy 40 GMRSPPVDRIDARNGEESTRTPLPGAPRREAAPVCCSARYNLLAFAQGFFIVYALRV 99  
Db 89 GMVSPPVDRIDARNGEESTRTPLPGAPRREAAPVCCSARYNLLAFAQGFFIVYALRV 148  
Qy 100 NLSVALVMDNSNTLEDNRTSKACPEHSAPIKVHNQDAETQWILGSQVASTPARY 159  
Db 149 NLSVALVMDNSNTLEDNRTSKACPEHSAPIKVHNQDAETQWILGSQVASTPARY 208  
Qy 160 YITQIPIGSYVASKGGKMLIGFGGIGLTGTAUTLTFPIAALDGVGLIVRLALEGGT 219  
Db 209 YITQIPIGSYVASKGGKMLIGFGGIGLTGTAUTLTFPIAALDGVGLIVRLALEGGT 268  
Qy 220 FPMHAMMSSWAPPERSKLLSISYAGAQGTVVISLPGSLICYMNWTVYFFGTIGI 279  
Db 269 FPMHAMMSSWAPPERSKLLSISYAGAQGTVVISLPGSLICYMNWTVYFFGTIGI 328  
Qy 280 FWFLLWIVLWISDTPOKHKRISHKEYVILSSLRNQLSQKSPVWPLKSLPQADNLRAKWNFST 339  
Db 329 FWFLLWIVLWISDTPOKHKRISHKEYVILSSLRNQLSQKSPVWPLKSLPQADNLRAKWNFST 388  
Qy 340 FSYNTWTFYLTLLIPTYMKRILRFNQVQENGLPSSLPYLGSLCMLLSQADNLRAKWNFST 399  
Db 389 FSYNTWTFYLTLLIPTYMKRILRFNQVQENGLPSSLPYLGSLCMLLSQADNLRAKWNFST 448  
Qy 400 STLCYRRFSLIGMGPVFLVAGFICGCSYSLAVAFLTSTLGFCSSGFSINHLDIA 459  
Db 449 STLCYRRFSLIGMGPVFLVAGFICGCSYSLAVAFLTSTLGFCSSGFSINHLDIA 508

RESULT 3  
US-09-359-167-2  
Sequence 2, Application US/09359167  
Patent No. 680448  
GENERAL INFORMATION:  
APPLICANT: Hellbergquist, Carl  
TITLE OF INVENTION: GBS Toxin Receptor  
FILE REFERENCE: CARB-008/1105  
CURRENT APPLICATION NUMBER: US/09/359, 167  
CURRENT FILING DATE: 1999-07-21  
EARLIER APPLICATION NUMBER: 60-693, 843  
EARLIER FILING DATE: 1998-07-22  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO: 2  
LENGTH: 495  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-359-167-2

Query Match 92.4%; Score 2621; DB 4; Length 495;  
Best Local Similarity 100.0%; Pred. No. 6.4e-271; Mismatches 0; Indels 0; Gaps 0;

Qy 42 MRSPPVDRIDARNGEESTRTPLPGAPRREAAPVCCSARYNLLAFAQGFFIVYALRVNL 101  
Db 1 MRSPPVDRIDARNGEESTRTPLPGAPRREAAPVCCSARYNLLAFAQGFFIVYALRVNL 60  
Qy 102 SYALVMDNSNTLEDNRTSKACPEHSAPIKVHNQDAETQWILGSQFYGYI 161  
Db 61 SYALVMDNSNTLEDNRTSKACPEHSAPIKVHNQDAETQWILGSQFYGYI 120  
Qy 162 ITQIPIGGYVASKGGKMLIGFGGIGLTGTAUTLTFPIAALDGVGLIVRLALEGGT 221  
Db 121 ITQIPIGGYVASKGGKMLIGFGGIGLTGTAUTLTFPIAALDGVGLIVRLALEGGT 180  
Db 222 ANHAMMSSWAPPERSKLLSISYAGAQGTVVISLPGSLICYMNWTVYFFGTIGFW 281  
Db 181 ANHAMMSSWAPPERSKLLSISYAGAQGTVVISLPGSLICYMNWTVYFFGTIGFW 240  
Qy 282 FLLWIVLWISDTPOKHKRISHKEYVILSSLRNQLSQKSPVWPLKSLPQADNLRAKWNFST 341  
Db 241 FLLWIVLWISDTPOKHKRISHKEYVILSSLRNQLSQKSPVWPLKSLPQADNLRAKWNFST 360  
Qy 402 LCYRRFSLIGMGPVFLVAGFICGCSYSLAVAFLTSTLGFCSSGFSINHLDIA 461  
Db 361 LCYRRFSLIGMGPVFLVAGFICGCSYSLAVAFLTSTLGFCSSGFSINHLDIA 420  
Qy 462 YAGILGTTNTFATIPGMVGPVIAKSLTPDNTVGBWOTVYIAAAINVFGAIFFLFAKG 521  
Db 421 YAGILGTTNTFATIPGMVGPVIAKSLTPDNTVGBWOTVYIAAAINVFGAIFFLFAKG 480  
Qy 522 EVQNWLNDHGHFRH 536  
Db 481 EVQNWLNDHGHFRH 495

RESULT 4

GenCore version 5.1.6						
Copyright (c) 1993 - 2005 Compugen Ltd.						
protein - protein search, using sw model						
on:	July 9, 2005, 05:11:02 ;	Search time 116.974 Seconds				
		(without alignments)				
	1772.2222 Million cell updates/sec					
file:	US-09-776-865-2					
Effect score:	2836					
Average:	1 MARGAMTPPRPVOPARPGGF.....LIFAKGEVQNWLNDHGHHRH 536					
String table:	BLOSUM62					
	Gapop 10.0 , Gapext 0.5					
Searched:	210592 seqs, 386760381 residues					
Number of hits satisfying chosen parameters:	2105692.					
Maximum DB seq length:	0					
Maximum DB seq length:	20000000000					
Post-processing:	Minimum Match 0%					
	Maximum Match 100%					
	Listing first 45 summaries					
Database :	A_Geneseq_16Feb04.*					
	1: geneseqp1980s:*					
	2: geneseqp1990s:*					
	3: geneseqp2000s:*					
	4: geneseqp2001s:*					
	5: geneseqp2002s:*					
	6: geneseqp2003as:*					
	7: geneseqp2003bs:*					
	8: geneseqp2004s:*					
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	XX					
SUMMARIES						
built	Score	Query	Match	Length	DB	ID
No.						
1	2836	100.0	536	3	AY450589	
2	2836	100.0	536	4	AAE06518	Aay*5089 Human GBS
3	2621	92.4	495	4	AY45087	Aae06518 Human gro
4	2621	92.4	495	4	AB66967	Aay45087 Partial h
5	2621	92.4	495	8	ADJ75516	Aab66967 Human AST
6	2621	92.4	495	8	ADP14587	Adj75516 Marker ge
7	2621	92.4	495	8	ADP25217	Adr14587 Human NF-
8	2614	92.2	495	4	ARM38959	Adp25217 PRO polyp
9	2329	82.1	495	4	AAY45088	Aam38959 Human pol
10	2329	82.1	495	4	AAE06519	Aay45088 Sheep GBS
11	1698	59.9	495	3	AY45050	Aae06519 Sheep gro
12	1679	59.2	314	8	AG365238	Aay450500 Human She
13	1614	56.9	309	4	AM40745	Aag365238 Human sod
14	1521	53.6	284	5	ABP41345	Aam40745 Human pol
15	1451	51.2	272	5	ABBB8975	Abp41345 Human ova
16	1450	51.1	277	4	ABBB8975	Abb8975 Human pol
17	1450	51.1	277	8	ADL32036	Aam931914 Human pol
18	996.5	35.1	559	4	ABBS8701	Adl32036 Human pro
19	992	35.0	502	4	ABBB65873	Abbs8701 Drosophil
20	992	35.0	502	4	ABBB65873	Abb65873 Drosophil
21	987	34.8	493	8	ADN21361	Abb65873 Drosophil
22	970	34.2	578	7	ADG88331	Adn21361 Bacter
23	970	34.2	582	6	ABG74796	Adg88331 Rat trans
24	970	34.2	582	6	ABG74797	Abg74796 Rat DNPI
25	970	34.2	582	6	ABM0487	Abg74797 Murine DN
						Abm0487 Rat Na-de
						Abh4787 Rat Na-de
						Abp41345 Human gro
						Abp41345 Human ova
						Abb8975 Human pol
						Abbs8701 Drosophil
						Abb65873 Drosophil
						Adn21361 Bacter
						Adg88331 Rat trans
						Abg74796 Rat DNPI
						Abg74797 Murine DN
						Abm0487 Rat Na-de
						Abh4787 Rat Na-de
						Abp41345 Human gro
						Abp41345 Human ova
						Abb8975 Human pol
						Abbs8701 Drosophil
						Abb65873 Drosophil
						Adn21361 Bacter
						Adg88331 Rat trans
						Abg74796 Rat DNPI
						Abg74797 Murine DN
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						Abh4787 Rat Na-de
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						Abg74797 Murine DN
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						Adn21361 Bacter
						Adg88331 Rat trans
						Abg74796 Rat DNPI
						Abg74797 Murine DN

PT	Modified-site	1336. .139	CC receptor and its fragments. Detecting the receptor in tissues is used to
PT		/note= "Asn is N-glycosylated"	CC diagnose pathological vascularisation, e.g. for detecting cancer
PT	Modified-site	1338. .141	CC metastases. GBS toxin receptors are useful for treating conditions
PT	Modified-site	138. .140	CC associated with pathological angiogenesis or neovascularisation
PT		/label= "Putative amidation site"	CC (specifically cancer, reperfusion injury, scarring during wound healing,
PT	Modified-site	167. .172	CC keloids, chronic inflammation (rheumatoid arthritis or psoriasis) or
PT		/note= "Putative phosphorylation site"	CC neural injury), and to raise specific antibodies used for treating early
PT	Modified-site	183. .188	CC onset disease. Inhibitors of this receptor are useful for treating
PT		/note= "Putative myristylation site"	CC pathological or hypoxia-induced endothelial cell proliferation and
PT	Modified-site	213. .218	CC migration.
PT	Modified-site	246. .251	CC
PT	Modified-site	250. .255	XX Sequence 536 AA;
PT	Modified-site	266. .269	Query Match 100.0%; Score 2836; DB 3; Length 536;
PT	Modified-site	297. .300	Best Local Similarity 100.0%; Prod. No. 1.5e-282;
PT	Modified-site	/label= "CAMP Phospho site	Matches 536; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
PT	Modified-site	300. .303	Qy 1 MAAGAMTPPRPVQPARPGFFGLSGRSRSLICQAVASTPAVGVRSVPVDRILARNDGEESTDR 60
PT	Modified-site	/label= "CK2 phospho site"	Db 1 MAAGAMTPPRPVQPARPGFFGLSGRSRSLICQAVASTPAVGVRSVPVDRILARNDGEESTDR 60
PT	Modified-site	310. .312	61 TPLPGAPAAEAVC5ARYNAILAFLGFFIYVARYNVLSTALVDRVDSNTTLEIDNRT 120
PT	Modified-site	/label= "PKC phospho site	61 TPLPGAPAAEAVC5ARYNAILAFLGFFIYVARYNVLSTALVDRVDSNTTLEIDNRT 120
PT	Modified-site	317. .320	Qy 121 SKACPEHSAPIKV/HNNQTCGKCYQDAETQWGLGSFPGYIITQIPIGGYVASKIGGKML 180
PT	Modified-site	/note= "Putative phosphorylation site"	Db 121 SKACPEHSAPIKV/HNNQTCGKCYQDAETQWGLGSFPGYIITQIPIGGYVASKIGGKML 180
PT	Modified-site	343. .346	Qy 181 GFGILGTAVLTLETFPIAADLGVPGLIVRALEGIGEVTFPAMHAWSSWAPPERSKIL 240
PT	Modified-site	/note= "Asn is N-glycosylated"	Db 181 GFGILGTAVLTLETFPIAADLGVPGLIVRALEGIGEVTFPAMHAWSSWAPPERSKIL 240
PT	Modified-site	378. .383	Qy 241 SISAGAOLGTIVSPLSGTICYYMNWVYFEGTIGFWFLWIVLWIVSDTQKRHS 300
PT	Modified-site	398. .401	Db 241 SISAGAOLGTIVSPLSGTICYYMNWVYFEGTIGFWFLWIVLWIVSDTQKRHS 300
PT	Modified-site	427. .432	Qy 301 HYEKEYILSSLRQLQSLQSQK5VPVNPVPIKSLPLMIAVVAHFSYNTWPTYLTLPTYMKBI 360
PT	Modified-site	444. .449	Db 301 HYEKEYILSSLRQLQSLQSQK5VPVNPVPIKSLPLMIAVVAHFSYNTWPTYLTLPTYMKBI 360
PT	Modified-site	464. .469	Qy 361 LRFNQENGFLSSLPYLGSLWCMILSGQADNLRAKNNFSTLCVRRISLGMIGPAVFL 420
PT	Modified-site	468. .473	Db 361 LRFNQENGFLSSLPYLGSLWCMILSGQADNLRAKNNFSTLCVRRISLGMIGPAVFL 420
PT	Modified-site	493. .496	Qy 421 VAAGFIGCDYSLAVAFLTSTLGGFCSSGSFSINHLDAPSAYGILGLGTNTPATPGIV 480
PT	Modified-site	/label= "CK2 phospho site"	Db 421 VAAGFIGCDYSLAVAFLTSTLGGFCSSGSFSINHLDAPSAYGILGLGTNTPATPGIV 480
PT		/note= "Putative phosphorylation site"	Qy 481 GPVIAKSLTPDNTFGEWQTVFVIAAAINVFGAIFTFLPAKGEVONWALNDHGHGRH 536
XX	PN	W200005375-A1.	Db 481 GPVIAKSLTPDNTFGEWQTVFVIAAAINVFGAIFTFLPAKGEVONWALNDHGHGRH 536
XX	PD	03-FEB-2000.	RESULT 2
XX	PP	22-JUL-1999;	AAE06518 standard; protein; 536 AA.
XX	PR	22-JUL-1998;	ID AAE06518;
XX	PA	(UYVA-) UNIV VANDERBILT.	AC XX
XX			XX
XX			DT 16-OCT-2001 (first entry)
XX			DE Human group B beta-haemolytic Streptococci toxin receptor (HP59) protein.
XX			KW Human; group B beta-haemolytic Streptococci toxin receptor; GBS; HP59;
PT			KW cytosstatic; vulnerable; antiatherosclerotic; osteopathic; vasoactive;
PT			KW prevention; attenuation; pathoangiogenic condition; cancer; scar;
XX			KW wound healing; gliosis; nerve injury; chronic wound; reperfusion injury;
XX			KW keloid; rheumatoid arthritis; atherosclerosis; osteoarthritis; psoriasis;
XX			KW vaccine.
PS			XX Homo sapiens.
XX			CC The present sequence is partial human GBS (group B beta-haemolytic
CC			CC streptococci) toxin receptor (HP55). GBS toxin receptor is an integral
CC			CC protein with seven transmembrane domains. Expression vectors comprising
CC			the coding region can be transformed into host cells to express GBS toxin